

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2003, 19:47:50 ; Search time 131 Seconds
(without alignments)
9378.222 Million cell updates/sec

Title: US-09-424-686B-1DEL

Perfect score: 4006

Sequence: 1 gtttcagcgagcgctgcgtc.....aaaaaaaaaaaaaaaaaaaa 4006

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_NA:*
2: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3982.6	99.4	4037	US-08-974-549A-343	Sequence 343, App
2	3969	99.1	4015	US-08-851-843A-224	Sequence 224, App
3	3969	99.1	4015	US-08-974-549A-1	Sequence 1, Appli
4	3969	99.1	4015	US-08-854-050-224	Sequence 224, App
5	3969	99.1	4015	US-09-430-323-224	Sequence 224, App
6	3969	99.1	4015	US-09-572-423B-3	Sequence 3, Appli
7	3969	99.1	4015	US-09-128-354-1	Sequence 1, Appli
8	3969	99.1	4015	US-09-675-321-1	Sequence 1, Appli
9	3969	99.1	4015	US-09-052-919-1	Sequence 173, App
10	3832.6	95.7	4029	US-08-851-843A-173	Sequence 173, App
11	3832.6	95.7	4029	US-08-974-549A-292	Sequence 292, App
12	3832.6	95.7	4029	US-08-854-050-173	Sequence 173, App
13	3832.6	95.7	4029	US-09-430-323-173	Sequence 173, App
14	3797	94.8	3855	US-08-974-549A-4	Sequence 4, Appli
15	2170.4	54.1	3451	US-08-974-549A-721	Sequence 721, App
16	2169.2	53.9	3396	US-08-974-549A-639	Sequence 639, App
17	2160.2	53.9	3396	US-08-974-549A-638	Sequence 638, App
18	2116.4	52.8	2176	US-08-851-843A-3	Sequence 3, Appli
19	2039.2	50.9	2171	US-08-851-843A-100	Sequence 100, App
20	2039.2	50.9	2171	US-08-974-549A-266	Sequence 266, App
21	2039.2	50.9	2171	US-08-854-050-100	Sequence 100, App
22	2039.2	50.9	2171	US-09-430-323-100	Sequence 100, App
23	1830.6	45.7	3396	US-08-974-549A-642	Sequence 642, App
24	1724.4	43.0	3396	US-08-974-549A-641	Sequence 641, App
25	1635.2	40.8	4335	US-08-974-549A-6	Sequence 6, Appli
26	1512.2	37.7	3396	US-08-974-549A-640	Sequence 640, App
27	427.2	10.7	44377	US-08-804-227C-7	Sequence 7, Appli

28	427.2	10.7	44377	2	US-08-804-198-1	Sequence 1, Appli
29	425.6	10.6	68750	3	US-09-335-409-1	Sequence 1, Appli
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36	425.6	10.6	71989	4	US-09-443-501A-2	Sequence 2, Appli
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38	412	10.3	38506	3	US-09-320-878-19	Sequence 1, Appli
39	410.8	10.3	43280	2	US-08-804-227C-1	Sequence 2, Appli
40	410.6	10.2	53526	3	US-08-658-136-2	Sequence 1, Appli
41	410.6	10.2	53577	3	US-08-658-136-1	Sequence 2, Appli
42	399.8	10.0	44377	2	US-08-804-227C-7	Sequence 7, Appli
43	399.8	10.0	44377	2	US-08-804-198-1	Sequence 1, Appli
44	399.4	10.0	36778	4	US-09-105-537-5	Sequence 5, Appli
45	397.6	9.9	43280	2	US-08-804-227C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-974-549A-343
; Sequence 343, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /note= "refined sequence of hTRT cDNA"
US-08-974-549A-343

Query Match 99.4%; Score 3982.6; DB 4; Length 4037;
Best Local Similarity 98.9%; Pred. No. 1.2e-235;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;

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RESULT 3

US-08-974-549A-1

; Sequence 1, Application US/08974549A

; Patent No. 616178

; GENERAL INFORMATION:

; APPLICANT: Cecch, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.

;; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
;; NUMBER OF SEQUENCES: 727
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/974,549A
;; FILING DATE: 19-NOV-1997
;; CLASSIFICATION: 536
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
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;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 1:
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;; TYPE: nucleic acid
;; STRANDEDNESS: single
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;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 56..3454
;; OTHER INFORMATION: /product= "hTERT"
;; OTHER INFORMATION: /note= "human telomerase reverse
;; OTHER INFORMATION: transcriptase (hTERT) catalytic protein
;; OTHER INFORMATION: component"
;; US-08-974-549A-1

Query Match

Best Local Similarity 99.1%; Score 3969; DB 4; Length 4015;
99.1%; Pred. No. 8e-235;

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QY	128	GCGGCTGCGCAGCTGCTGCGCAGCTGGGAAGCCCTGGCCCCGGCCACCCCGCGATG	187		
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RESULT 4
US-08-854-050-224
; Sequence 224, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111

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RESULT 5
 US-09-430-323-224
 Sequence 224, Application US/09430323
 Patent No. 6309867
 GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: No. 6309867el Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/430,323
 FILING DATE: 29-Oct-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429

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REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-430-323-224
Query Match 99.1%; Score 3969; DB 4; Length 4015;
Best Local Similarity 99.1%; Pred. No. 8e-235;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps
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QY 368 GCTGCTGAGCGGGGCGCGCGGGGGCGCGCGAGGCGCTTCAACCAACAGCGTGGCGACGTA 427
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Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGACACTTGAAGAGGGTGACGTGCGGAGCTGTC	1860
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QY	3272	GACTCGACACCGTGTACACTGCTGCGCACTCTCTGGGGTCACTCAGACAGCAGCCAGACGCA	3331
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QY	3332	GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCTGCCCTGGAGGCGCAGGCCAACCCGCG	3391
Db	3361	GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCTGCCCTGGAGGCGCAGGCCAACCCGCG	3420
QY	3392	ACTGCCCTCAGACTTCAAGACCAATCCTGAGTGTGAGGCTGAGGCCAACCCGCCACAGGCCGA	3451
Db	3421	ACTGCCCTCAGACTTCAAGACCAATCCTGAGTGTGAGGCTGAGGCCAACCCGCCACAGGCCGA	3480
QY	3452	GAGCAGACACCAAGACGCGCTGTCAAGCCCGGGCTCTACGTCCAGAGGAGGAGGGGGCGGC	3511
Db	3481	GAGCAGACACCAAGACGCGCTGTCAAGCCCGGGCTCTACGTCCAGAGGAGGAGGGGGCGGC	3540
QY	3512	CACACCCAGGCGCCGACCGCTGGGAGTCTGAGGCTGAGTGTGAGTGTGAGGCGCGAGGCGCTG	3571
Db	3541	CACACCCAGGCGCCGACCGCTGGGAGTCTGAGGCTGAGTGTGAGTGTGAGGCGCGAGGCGCTG	3600
QY	3572	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG	3631
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG	3660
QY	3632	GAGTGTCCAGACACCTGCGCTTCTCACTTCCACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG	3691
Db	3661	GAGTGTCCAGACACCTGCGCTTCTCACTTCCACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG	3720
QY	3692	GGGCGAGCTTTTCTTCAACAGAGGCGCGGCTTCCATCCCAATAGGAATAGTCCATCC	3751
Db	3721	GGGCGAGCTTTTCTTCAACAGAGGCGCGGCTTCCATCCCAATAGGAATAGTCCATCC	3780
QY	3752	CCAGATTGCGCATTTGTTCAACCCCTGCGCCCTGCTTGGCTTCCACCCCAACCATCC	3811
Db	3781	CCAGATTGCGCATTTGTTCAACCCCTGCGCCCTGCTTGGCTTCCACCCCAACCATCC	3840
QY	3812	AGGTGAGAGCCCTGAGAAAGGACCCCTGCACTGTGATGGGGTCCCTGTGGTCAAAATGGGG	3871
Db	3841	AGGTGAGAGCCCTGAGAAAGGACCCCTGCACTGTGATGGGGTCCCTGTGGTCAAAATGGGG	3900
QY	3872	CCCGTACACAGGCGAGGACCCCTGCACTGTGATGGGGTCCCTGTGGTCAAAATGGGG	3931
Db	3901	CCCGTACACAGGCGAGGACCCCTGCACTGTGATGGGGTCCCTGTGGTCAAAATGGGG	3960
QY	3932	GAGTGTCTGTGGAGTAAATATCTGAATATATAGAGTTTTCAGTTTGAAGAAAAA	3986
Db	3961	GAGTGTCTGTGGAGTAAATATCTGAATATATAGAGTTTTCAGTTTGAAGAAAAA	4015

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RESULT 6
US-09-572-423B-3
; Sequence 3, Application US/09572423B
; Patent No. 6331399
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William A. Gaarde
; APPLICANT: Edward Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0462
; CURRENT APPLICATION NUMBER: US/09/572,423B
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-572-423B-3

Query Match          99.1%; Score 3969; DB 4; Length 4015;
Best Local Similarity 99.1%; Pred. No. 8e-235;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY      8 GCAGCGCTGCGTCCGTGCTGGCAGACGTGGGAAGCCCTGGGCCCGGCACCCCGCGATGCC 67
Db       1 GCAGCGCTGCGTCTGCTGCTGGCAGACGTGGGAAGCCCTGGGCCCGGCACCCCGCATGCC 60

QY      68 GCGCGCTCCCGCGCTGCGAGCCGTGCGCTCCCTGCTGTCGACAGCACTACC CGAGGTGCT 127
Db       61 GCGCGCTCCCCCGCTGCGAGCCGTGCGCTCCCTGCTGTCGAGCACCACTACC CGAGGTGCT 120

QY      128 GCCGCTGGCCACGTTCTGTGCGGGCGCCCTGGGGCCCCAGGGCTGGCGCTGTGCAAGCGCG 187
Db       61 GCGCGCTCCCCCGCTGCGAGCCGTGCGCTCCCTGCTGTCGAGCACCACTACC CGAGGTGCT 120

QY      121 GCCGCTGGCCACGTTCTGTGCGGGCGCCCTGGGGCCCCAGGGCTGGCGCTGTGCAAGCGCG 180
Db       121 GCCGCTGGCCACGTTCTGTGCGGGCGCCCTGGGGCCCCAGGGCTGGCGCTGTGCAAGCGCG 180

QY      188 GGACCCGCGGCTTTCGCGCGCGCTGTGGCCAGTGCTGCTGTGCTGCGCTGGACGC 247
Db       181 GGACCCGCGGCTTTCGCGCGCGCTGTGGCCAGTGCTGCTGTGCTGCGCTGGACGC 240

QY      248 ACGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 307
Db       241 ACGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 300

QY      308 CCGAGTGTGTCAGAGGCTGTGCGAGCGCGGGCGGGCGGCAAGAAGCTGTGCGCTTCGCTTCGC 367
Db       301 CCGAGTGTGTCAGAGGCTGTGCGAGCGCGGGCGGGCGGCAAGAAGCTGTGCGCTTCGCTTCGC 360

QY      368 GCTGCTGAGCGGGGGCGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 427
Db       361 GCTGCTGAGCGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420

QY      428 CCTGCCAACAACGCTGACCGACGACTGCGGGGGAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 487
Db       421 CCTGCCAACAACGCTGACCGACGACTGCGGGGGAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480

QY      488 CCGCGTGGGGCGACGAGCTGTGTTCAACCTGCTGGACGCTGCGCGCTTTTGTGCTGTGT 547
Db       481 CCGCGTGGGGCGACGAGCTGTGTTCAACCTGCTGGACGCTGCGCGCTTTTGTGCTGTGT 540

QY      548 GGCTCCAGCTGCGCTTACCAAGGTGTGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 607
Db       541 GGCTCCAGCTGCGCTTACCAAGGTGTGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 600

QY      608 TCAGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 667
Db       601 TCAGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 660

QY      668 CTGGAACCAATAGCTTCAGGGAAGGCGGGGGTCCCCCTGGGCTGCCAGCCCCGGGGTGCAG 727

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Db	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCTGGGCTGCCAGCCCCGGGTGCAG	720
QY	728	GAGCGCGGGGAGTGGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCCAAGCGCTGGCGC	787
Db	721	GAGCGCGGGGAGTGGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCCAAGCGCTGGCGC	780
QY	788	TGCCCTGAGCCGAGCGGAGCGCCCGTTGGGCAAGGGGTCTGGGCCACCCGGGCAGGAC	847
Db	781	TGCCCTGAGCCGAGCGGAGCGCCCGTTGGGCAAGGGGTCTGGGCCACCCGGGCAGGAC	840
QY	848	GCGTGACCGAGTGAACCGTGGTTCTGTGTGTACCTGCCAGACCCGCGAAGAAGC	907
Db	841	GCGTGACCGAGTGAACCGTGGTTCTGTGTGTACCTGCCAGACCCGCGAAGAAGC	900
QY	908	CACCTCTTTGAGGGGTGCGCTCTCTGGACAGCGCCACTCCACCACATCCGTTGGCCGCCA	967
Db	901	CACCTCTTTGAGGGGTGCGCTCTCTGGACAGCGCCACTCCACCACATCCGTTGGCCGCCA	960
QY	968	GCACACGCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGCCCTGTCC	1027
Db	961	GCACACGCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGCCCTGTCC	1020
QY	1028	CCCGGTGTACGCCCGAGACCAGCACTTCTTACTCTCAGGCGACAAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACGCCCGAGACCAGCACTTCTTACTCTCAGGCGACAAGAGCAGCTGCG	1080
QY	1088	GCCCTCCTTCTACTACGCTCTGTAGGCCCCAGCCTGACTGGCGCTCGAGCCTGTGA	1147
Db	1081	GCCCTCCTTCTACTACGCTCTGTAGGCCCCAGCCTGACTGGCGCTCGAGCCTGTGA	1140
QY	1148	GACCATCTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCGCCT	1207
Db	1141	GACCATCTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCTGTCTGTGAGCTGCTTGGGAACACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCTGTCTGTGAGCTGCTTGGGAACACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCAGC	1327
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCAGC	1320
QY	1328	AGCCGGTGTGTGCCCCGGGAGAAAGCCCCAGGGCTGTGGCGCCCCCGAGAGGAGA	1387
Db	1321	AGCCGGTGTGTGCCCCGGGAGAAAGCCCCAGGGCTGTGGCGCCCCCGAGAGGAGA	1380
QY	1388	CACAGACCCCCGTGCGCTGTGAGCTGCTCGCCAGCACAGACGCCCTGCGAGGTGA	1447
Db	1381	CACAGACCCCCGTGCGCTGTGAGCTGCTCGCCAGCACAGACGCCCTGCGAGGTGA	1440
QY	1448	CGGCTTGTGCGGGCTGCGCTGCGCGCGGTGTGGCCCCAGGCCCTGTGGGCTCCAGGCA	1507
Db	1441	CGGCTTGTGCGGGCTGCGCTGCGCGCGGTGTGGCCCCAGGCCCTGTGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGGCTTCCCTCAGGAACACCAAGAATTCATCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGGCTTCCCTCAGGAACACCAAGAATTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGTGCAGGAGTGAAGTGGAAAGTGAAGCGTGGGAGCTGCGCTTGGCTGCCAG	1627
Db	1561	GCTCTCGTGCAGGAGTGAAGTGGAAAGTGAAGCGTGGGAGCTGCGCTTGGCTGCCAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTCCGGCCGAGAGCACCGTCTGCGTGAGAGATCTGGC	1687
Db	1621	GAGCCCAAGGGGTGGCTGTGTCCGGCCGAGAGCACCGTCTGCGTGAGAGATCTGGC	1680
QY	1688	CAAGTTCCTGCACCTGGCTGTAGTGTGTACGTGCTGAGCTGCTCAGGCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACCTGGCTGTAGTGTGTACGTGCTGAGCTGCTCAGGCTTTCTTTTA	1740
QY	1748	TGTCACGGAGACACGTTTCAAAAGAACAGGCTTTTCTACCGGAAGATGTCTGGAG	1807

Db	1741	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTC	1800
QY	1808	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACCTTGAAGAGGTGCAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACCTTGAAGAGGTGCAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCGACGATCGGGAAAGCCAGGCCGCCCTGCTGACGTCACAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCGACGATCGGGAAAGCCAGGCCGCCCTGCTGACGTCACAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGGACTACGTCGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGGACTACGTCGTGGAGC	1980
QY	1988	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAAGGGTGAAGGCACGTGT	2047
Db	1981	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAAGGGTGAAGGCACGTGT	2040
QY	2048	CAGCGTGCCTCAACTACGAGCGCGCGCGCGGCCGCCCTCTCGGGCGCTGTGTGCTGGG	2107
Db	2041	CAGCGTGCCTCAACTACGAGCGCGCGCGCGGCCGCCCTCTCGGGCGCTGTGTGCTGGG	2100
QY	2108	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGCTGCGGGCCAGGACCC	2167
Db	2101	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGCTGCGGGCCAGGACCC	2160
QY	2168	GCCGCCCTGAGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGCGCTTACGACACCATCCCCCA	2220
QY	2192	GGACAGGCTCAGCGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTA	2251
Db	2221	GGACAGGCTCAGCGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTA	2280
QY	2252	TGCGTATGCCGTGGTCCAGAAAGGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCCA	2311
Db	2281	TGCGTATGCCGTGGTCCAGAAAGGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2312	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGATTCGTGGCTCACCTGCAGGA	2371
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGATTCGTGGCTCACCTGCAGGA	2400
QY	2372	GACCAGCCCGCTGAGGAGTGCCTGCTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG	2431
Db	2401	GACCAGCCCGCTGAGGAGTGCCTGCTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG	2460
QY	2432	CAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCACACAGCGCGTGCATCAGGGG	2491
Db	2461	CAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCACACAGCGCGTGCATCAGGGG	2520
QY	2492	CAAGTCTTACGTCACAGTGCAGGCGGATCCCGCAGAGGCTCCATCTCTCCACGCTGCTCG	2551
Db	2521	CAAGTCTTACGTCACAGTGCAGGCGGATCCCGCAGAGGCTCCATCTCTCCACGCTGCTCG	2580
QY	2552	CAGCCTGTGCTACGGCGACATGAGAACCAAGCTGTTGCGGGGATTCGGCGGGAGCGGGCT	2611
Db	2581	CAGCCTGTGCTACGGCGACATGAGAACCAAGCTGTTGCGGGGATTCGGCGGGAGCGGGCT	2640
QY	2612	GCTCTGCGCTTGTGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGCGAAAAAC	2671
Db	2641	GCTCTGCGCTTGTGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGCGAAAAAC	2700
QY	2672	CTTCTCAGGACCCCTGTGTCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTTGGCGAA	2731
Db	2701	CTTCTCAGGACCCCTGTGTCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTTGGCGAA	2760
QY	2732	GACAGTGTGAACCTTCCCTGTAGAAGCAGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGTGAACCTTCCCTGTAGAAGCAGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2820
QY	2792	GCCGCGCCACGGCCTATTTCCCTGTGTGCGGCCCTGCTGCTGATACCCGGAACCTTGAGGT	2851
Db	2821	GCCGCGCCACGGCCTATTTCCCTGTGTGCGGCCCTGCTGCTGATACCCGGAACCTTGAGGT	2880

QY 2852 GCAGAGCAGTACTTCCAGCTATGCCCCGACGCTCCATCAGAGCCAGTCTCACCCTTCAACCG 2911
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QY 2912 CGGCTTCAAGGCTGGGAGGAACATGCGTGCACAACTCTTTGGGGCTTTGGGGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTGCACAACTCTTTGGGGCTTTGGGGCTGAAGTG 3000
QY 2972 TCACAGCCCTGTTCTGATTTTGAGGTGACAGGCTCCAGAGGCTGTGACCAACATCTA 3031
Db 3001 TCACAGCCCTGTTCTGATTTTGAGGTGACAGGCTCCAGAGGCTGTGACCAACATCTA 3060
QY 3032 CAAGATCCCTGCTGTCAGGCGTACAGGTTTTCACGCAATGTGCTGCAGAGTCCCATTTCA 3091
Db 3061 CAAGATCCCTGCTGTCAGGCGTACAGGTTTTCACGCAATGTGCTGCAGAGTCCCATTTCA 3120
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QY 3152 CTGCTACTCATCTCTGAAAAGCCAAAGACGAGGATGTGCTGGGGCCCAAGGGCCGCGC 3211
Db 3181 CTGCTACTCATCTCTGAAAAGCCAAAGACGAGGATGTGCTGGGGCCCAAGGGCCGCGC 3240
QY 3212 CGGCCCTCTGCCCCCTCCGAGGCGCTGCAAGTGTGCTGACCAAGCATTTCTGCTCAAGCT 3271
Db 3241 CGGCCCTCTGCCCCCTCCGAGGCGCTGCAAGTGTGCTGACCAAGCATTTCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGTGTCTACCTACGTGACCTCTGCGGGTCTACTCAGAGACGCCAGACGCA 3331
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QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGGCCAAGGCT 3631
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QY 3632 GAGTGTCCAGACACACCTGCGTCTTCACTTCCACAGGCTGGCGCTCGGCTCCACCCCA 3691
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QY 3692 GGGCCAGCTTTTCTCTACCAAGAGGCGCGCTTCCACTCCCATAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTTCTCTACCAAGAGGCGCGCTTCCACTCCCATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTGCGCATTTGTTCACCCCTGCGCTTCCCTCTTTCCTTCCACCCCAACATCC 3811
Db 3781 CCAGATTGCGCATTTGTTCACCCCTGCGCTTCCCTCTTTCCTTCCACCCCAACATCC 3840
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QY 3872 CCCTGTACACAGGCGAGGACCCCTGCACCTGAGTGGGGGTCCCTGTGGGTCAAAATGGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGAGTGGGGGTCCCTGTGGGTCAAAATGGGGG 3960

QY 3932 GAGTGTCTGTGGAGTAATAATCTGATATATGAGTTTTTCAGTTTGAATAAAA 3986
Db 3961 GAGTGTCTGTGGAGTAATAATCTGATATATGAGTTTTTCAGTTTGAATAAAA 4015

RESULT 7
US-09-128-354-1
; Sequence 1, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-00310US
; CURRENT FILING DATE: 1998-08-03
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
; US-09-128-354-1

Query Match 99.1%; Score 3969; DB 4; Length 4015;
Best Local Similarity 99.1%; Pred. No. 8e-235;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCGGCAACCCCGCGATGCC 67
Db 1 GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCGGCAACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGCGAGCGGTGCGCTCCCTGCTGCGGACGACCTACCGCGAGGTGCT 127
Db 61 GCGCGCTCCCGCTGCGCGAGCGGTGCGCTCCCTGCTGCGGACGACCTACCGCGAGGTGCT 120
QY 128 GCGCGTGGCCACGTTGCTGCGCGGCGCTGGGGCCCGCAGGGGCTGGGTGTCAGCGCGG 187
Db 121 GCGCGTGGCCACGTTGCTGCGCGGCGCTGGGGCCCGCAGGGGCTGGGTGTCAGCGCGG 180
QY 188 GGAACCGGCGGCTTTCGCGCGGCTGTGCGCCAGTGTGCTGTGCGCTGGGAGAGTGTGCG 247
Db 181 GGAACCGGCGGCTTTCGCGCGGCTGTGCGCCAGTGTGCTGTGCGCTGGGAGAGTGTGCG 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCGCGCTTCCGCGAGGTGCTCTGAGAGAGTGTGCG 307
Db 241 ACGGCGCGCGCGCGCGCGCGCGCGCGCTTCCGCGAGGTGCTCTGAGAGAGTGTGCG 300
QY 308 CCGAGTGTCTGAGAGGCTGTGCGAGCGCGGCGGCGGAAGACGTGCTGGCTTGGCTTCCG 367

QY 2492 CAAGTCTACGTCCAGTGCAGAGGGATCCCGCAGGGCTCCATTCCTCTTCACGGCTGCTGTG 2551
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Db 2521 CAAGTCTACGTCCAGTGCAGAGGGATCCCGCAGGGCTCCATTCCTCTTCACGGCTGCTGTG 2580
QY 2552 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTTGCGGGATTTGCGGGAGCGGGCT 2611
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Db 2581 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTTGCGGGATTTGCGGGAGCGGGCT 2640
QY 2612 GCTCTGCGGTTTGGTGGATGATTTCTGTGTGTGACACCTTACCTCACCACGCGGAAAC 2671
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Db 2641 GCTCTGCGGTTTGGTGGATGATTTCTGTGTGTGACACCTTACCTCACCACGCGGAAAC 2700
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Db 2701 CTTCCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGCGTGCCTGTAACCTTGCAGAA 2760
QY 2732 GACAGTGTGTAATTTCCCTGTAGAAGACGAGCCCTGGGTGGACGGCTTTTGTTCAGAT 2791
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Db 2761 GACAGTGTGTAATTTCCCTGTAGAAGACGAGCCCTGGGTGGACGGCTTTTGTTCAGAT 2820
QY 2792 GCCGGCCACGCGCTATTCCCTGTGTCGCGCTGCTGCTGATACCCGAGCCCTGAGGT 2851
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Db 2821 GCCGGCCACGCGCTATTCCCTGTGTCGCGCTGCTGCTGATACCCGAGCCCTGAGGT 2880
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QY 2972 TCACAGCCTGTTCTTGATTTGACGTGAAACAGCCTCCACAGCGGTGTGCACCAACATCTA 3031
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Db 3001 TCACAGCCTGTTCTTGATTTGACGTGAAACAGCCTCCACAGCGGTGTGCACCAACATCTA 3060
QY 3032 CAAGATCTCTCTGTCGACGCGTACAGGTTTACGCATGTGTGTGACGCTCCATTTC 3091
|||||
Db 3061 CAAGATCTCTCTGTCGACGCGTACAGGTTTACGCATGTGTGTGACGCTCCATTTC 3120
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QY 3152 CTGCTACTCCATCTGAAAGCCAAAGAACGACGAGTGTGCTGGGGCCAAAGGCGCGC 3211
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QY 3212 CGGCCCTCTGCCCTCCGAGGCGGTGCACTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271
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Db 3241 CGGCCCTCTGCCCTCCGAGGCGGTGCACTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
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RESULT 8

US-09-675-321-1
; Sequence 1, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675,321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ. ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
US-09-675-321-1

Query Match 99.1%; Score 3969; DB 4; Length 4015;
Best Local Similarity 99.1%; Pred. No. 8e-235;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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RESULT 9

US-09-052-919-1

; Sequence 1, Application US/09052919

; Patent No. 6444650

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Compositions for Detecting and

; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/052,919

; FILING DATE: 31-MAR-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-0036000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FEATURE:
NAME/KEY: CDS
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OTHER INFORMATION: /product= "human telomerase reverse
OTHER INFORMATION: transcriptase (hTERT)"
US-09-052-919-1

Query Match 99.1%; Score 3969; DB 4; Length 4015;
Best Local Similarity 99.1%; Pred. NO. 8e-235;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTGCTGCTGCGACGTGGAGCCCTGGCCCCCGGCACACCCCGCATGCC 67
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DB 1201 GCGCGAGCGCTACTGCGAATGCGCGCGCGCTGTTCTGAGGCTGTGGAACCAAGCGCA 1260
QY 1268 GTGCGCTACGCGGGGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTCAACCCAGC 1327
DB 1261 GTGCGCTACGCGGGGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTCAACCCAGC 1320
QY 1328 AGCGGCTGTGTGCGCGCGGGAAGAGCCCGCAGGCTCTGTGCGGCGCGCGCGAGAGGAGA 1387

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Db 1321 AGCCGGTGTGTGTGCCCCGGAGAGAGCCCAAGGCTCTGTGGCGGCCCCCGAGAGAGAGGA 1380
QY 1388 CACAGACCCCCCGTGCCTGTGTGACAGTGTCTCCGACAGACAGACGCCCTGGCAGGTGTA 1447
Db 1381 CACAGACCCCCCGTGCCTGTGTGACAGTGTCTCCGACAGACAGACGCCCTGGCAGGTGTA 1440
QY 1448 CGGCTTCGTGGGGCCCTGGCTGGCCGGCTGGTGGCCCGACGCTCTGTGGGGCTCCAGGCA 1507
Db 1441 CGGCTTCGTGGGGCCCTGGCTGGCCGGCTGGTGGCCCGACGCTCTGTGGGGCTCCAGGCA 1500
QY 1508 CAACGACGCGCGTTCCTCAGGAACAACAAGATTCATCTCCCTGGGGAAGCATGCCAA 1567
Db 1501 CAACGACGCGCGTTCCTCAGGAACAACAAGATTCATCTCCCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCGTCAGAGAGTGCAGTGCAGATGAGCGTGCAGGACTGCGCTTGGCTGGCGAG 1627
Db 1561 GCTCTGCGTCAGAGAGTGCAGTGCAGATGAGCGTGCAGGACTGCGCTTGGCTGGCGAG 1620
QY 1628 GAGCCACGCGGTGGCTGTGTCCGGCCGACAGCACCGCTGCGGTGAGAGATCCTGGC 1687
Db 1621 GAGCCACGCGGTGGCTGTGTCCGGCCGACAGCACCGCTGCGGTGAGAGATCCTGGC 1680
QY 1688 CAAGTTCCTGCAGTGCCTGATGATGTGTACGTCTGTGAGCTGCTCAGGTCCTTTTAA 1747
Db 1681 CAAGTTCCTGCAGTGCCTGATGATGTGTACGTCTGTGAGCTGCTCAGGTCCTTTTAA 1740
QY 1748 TGTACGAGAGACACAGCTTCAAAAAGACAGGCTCTTTTCTACCGGAAGATGTCTGAG 1807
Db 1741 TGTACGAGAGACACAGCTTCAAAAAGACAGGCTCTTTTCTACCGGAAGATGTCTGAG 1800
QY 1808 CAAGTTGCAAGCATTTGGAATCAGACAGACTTGAAGAGGTTGCAGCTGGGAGGCTGTC 1867
Db 1801 CAAGTTGCAAGCATTTGGAATCAGACAGACTTGAAGAGGTTGCAGCTGGGAGGCTGTC 1860
QY 1868 GGAAGCAGAGGTTCAGGACATCGGGAAGCCAGGCCGCGCTGCTGACGTCACAGACTCCG 1927
Db 1861 GGAAGCAGAGGTTCAGGACATCGGGAAGCCAGGCCGCGCTGCTGACGTCACAGACTCCG 1920
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Db 1921 CTTCATCCCAAGCCTGACGGGCTGCGGCCGATGTGAAATGAGACTGCTGTGGAGC 1980
QY 1988 CAGAACGTTCCGACAGAAAAGAGGCGCAGCGTCTACCTCGAGGGTTGAAGGCACCTGTT 2047
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Db 2101 CGTGAGCAGATTCACAGGGGCTGCGCACCTTCTGCTGCTGTGTGGGGCCAGAGACC 2160
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Db 2161 GCCGCTGAGCTGTACTTGTCAAGGTGATGTGACGGCGCGTACGACACCATCCCCCA 2220
QY 2192 GGACAGGCTCAGGAGGTCTATCGCCACGATCAAAACCCAGAAACGTAAGTGTGGC 2251
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QY 2312 CGTCTACCTTGACAGACTTCAGCGCGTACATGGACAGTGTGTGGCTACCTGAGGA 2371
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QY 2492 CAAGTCTTACGTCAGTTCAGAGGATCCCGCAGGGCTCCATCTCTTCCACGCTGCTCTG 2551
Db 2521 CAAGTCTTACGTCAGTTCAGAGGATCCCGCAGGGCTCCATCTCTTCCACGCTGCTCTG 2580
QY 2552 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTGGGGGATTCGGCGGAGCGGCT 2611
Db 2581 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTGGGGGATTCGGCGGAGCGGCT 2640
QY 2612 GCTCCTGCGTTGGTGTGATGATTTCTTGTGTGACACCTCACCCTCACCCAGCGAAAC 2671
Db 2641 GCTCCTGCGTTGGTGTGATGATTTCTTGTGTGACACCTCACCCTCACCCAGCGAAAC 2700
QY 2672 CTTCCTCAGGACCCCTGGTCCGAGGTGTCCTGATGAGGCTGCGGTGAACCTTGGGAA 2731
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QY 2732 GACAGTGTGAACCTTCCCTGTAGAAACGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT 2791
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QY 2792 GCCGGCCCCACGGCTATTCGCCCTGTGTGGCGCTGCTGTGATATCCCGGACCTGGAGGT 2851
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QY 2912 CGGCTTCAAGGCTGGGAGGAACATGCGTGCACAACTCTTTGGGGCTTTCGGGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTGCACAACTCTTTGGGGCTTTCGGGCTGAAGTG 3000
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Db 3121 TCAGCAAGTTTGGAAAGAACCCACATTTTCTGCGGCTATCTGTGACACAGGCTCCCT 3180
QY 3152 CTGCTACTCCATCTTGAAGAACCCAAAGAACGACAGGATGTGCTGGGGCCAAAGGCGCCG 3211
Db 3181 CTGCTACTCCATCTTGAAGAACCCAAAGAACGACAGGATGTGCTGGGGCCAAAGGCGCCG 3240
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Db 3241 CGGCCCTGTGCCCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCATTCCTGTCAAGCT 3300
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QY 3512 CACACCCAGGCCCCGACCCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCTG 3571
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QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGTGTCCAGCCAGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGTGTCCAGCCAGGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGCTCTTCACTTCCACAGGCTGCGCTGCGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGCTCTTCACTTCCACAGGCTGCGCTGCGCTCCACCCCA 3720
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QY 3812 AGGTGAGACCTGAGAAGGACCCCTGGAGCTTGGAATTTGAGTGAACAAAGGTGTG 3871
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QY 3932 GAGGTGCTGTGGAGTAAATATGATGATTTTCACTTTTGAATAAAAA 3986
Db 3961 GAGGTGCTGTGGAGTAAATATGATGATTTTCACTTTTGAATAAAAA 4015

RESULT 10
US-08-851-843A-173
; Sequence 173, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: LOCATION: 1..4029
OTHER INFORMATION: /note="preliminary sequence for
OTHER INFORMATION: human TRT cDNA insert of
OTHER INFORMATION: plasmid pGRN121"
US-08-851-843A-173

Query Match 95.7%; Score 3832.6; DB 3; Length 4029;
Best Local Similarity 97.9%; Pred. No. 1.6e-226;
Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;
QY 8 GCAGCGCTGCGTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCGCGCACCCCGGATGCC 67
Db 1 GCAGCGCTGCGTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCGCGCACCCCGGATGCC 60
QY 68 GCGGCTCCCGCTGCGGAGCCGCTGCTGCTGCGCAGCCACTACCGGAGGTGCT 127
Db 61 GCGGCTCCCGCTGCGGAGCCGCTGCTGCTGCGCAGCCACTACCGGAGGTGCT 120
QY 128 GCCGCTGCCAGCTTCTGTCGCGGCGCTGGGGCCCCAGGGCTGGCGCTGTCAGCGCG 187
Db 121 GCCGCTGCCAGCTTCTGTCGCGGCGCTGGGGCCCCAGGGCTGGCGCTGTCAGCGCG 180
QY 188 GGACCCGGGCTTTCGCGCGCTGTCGCGCCAGTGCCTGTGCTGCCCTGGAGCC 247
Db 181 GGACCCGGGCTTTCGCGCGCTGTCGCGCCAGTGCCTGTGCTGCCCTGGAGCN 240
QY 248 ACGGCGGCCCCCGGCGGCCCCCTCTCTCCGCCAGGTGTCCTGCTGAAGAGCTGTGCC 307
Db 241 ACGGCGGCCCCCGGCGGCCCCCTCTCTCTCCGCCAGGTGTCCTGCTGAAGAGCTGTGCC 300
QY 308 CCGAGTCTGAGAGGCTGTGCGAGCGCGGCGGCGGAAGACGTGTGCGCTTGGCTTCCG 367
Db 301 CCGAGTCTGAGANANGCTGTGCGAGCGGCGGCGGAANACGTGTGCGCTTGGCTTCCG 360
QY 368 GCTGTGAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTA 427
Db 361 GCTGTGAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTA 420
QY 428 CCTGCCAAGAGGCTGACCGACGCTGCGGGGAGCGGGGCGGCTGCTGCTGCG 487
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Db 541 GCGTCCAGCTGCGCTACAGAGGTGTGCGGGGCGGCGGCTGTACAGCTGCGGCTGCNAC 600
QY 608 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 667
Db 601 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 658

Db 2813 GATGCCGGCCACGGCCCTATTCCCTGGTGGCCCTGCTGCTGATATACCCGGACCTGGA 2872

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Db 3173 CCTCTGCTACTCCATCTCTGAAGAACCAAGAACCGCAGAGGATGTGCTGGGGCCAAAGGCGC 3232

QY 3209 CGCCGGCCCTCTGCCCCCTCCAGAGCCGCTGACAGTGGCTGTGCCAACCAAGCATTCCTGCTCAA 3268

Db 3233 CGCCGGCCCTCTGCCCCCTCCAGAGCCGCTGACAGTGGCTGTGCCAACCAAGCATTCCTGCTCAA 3292

QY 3269 GCTGACTCGACACCCGTTGTCACTACCTACGTGCCACTCTGGGGTCACTCAGAGACAGCCAGAC 3328

Db 3293 GCTGACTCGACACCCGTTGTCACTACCTACGTGCCACTCTGGGGTCACTCAGAGACAGCCAGAC 3352

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Db 3353 GCAGCTGAGTCGGAAGCTCCCGGGGAGCAGCTGACTGCCCTGAGAGCCGACAGCCAAACC 3412

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QY 3509 GCCCACACCCAGGCCCCGACCCGCTGGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGC 3568

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QY 3569 CTGCAATCTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAG 3628

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Db 3653 GCTGAGTGTCCAGCACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGCTGCCACC 3712

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QY 3749 TCCCCAGATTGCCATGTTCACCCCTGCGCTTCCCTTCCCTTCCACCCCCACCA 3808

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Db 3833 TCCAGGTGAGAGCCCTGAGAAGAGACCTGGGAGCTCTGGGAATTTGAGTGAACCAAAAGT 3892

QY 3869 GTGCCCTGTACACAGGCGAGAGACCTGCACTGGATGGGGTCCCTGTGGTCAAAATTGG 3928

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Db 4013 AAAAAAAAAAAAAA 4029

RESULT 11

US-08-974-549A-292

; Sequence 292, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

QY 1865 GTCGGAAGCAGAGGTCAAGGCAGCATCGGGAAGCCAGCCCCGCTGCTGACGTCCAGACT 1924
|||||
Db 1853 GTCGGAAGCAGAGGTCAAGGCAGCATCGGGAAGCCAGCCCCGCTGCTGACGTCCAGACT 1912
QY 1925 CCGCTTCATCCCCCAAGCCTGACGGGCTGCGCCGATTTGTGAACATGACTACGTCTGGG 1984
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QY 2309 CCACGCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGCTCACTGCA 2368
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Db 2333 CCACGCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGCTCACTGCA 2392
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Db 2453 CAGCAGTGGCTCTTGCGACGTCTTCTACGCTTATGTGCCACCAAGCCGTGCGCATCAG 2512
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Db 2513 GGGCAAGTCTTAAGTCCAGTGGCAGAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCT 2572
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Db 2633 GCTGCTCTGCGTTTGGTGAATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAA 2692
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Db 2693 AACCTTCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGGCTGCGTGTGAATTGCG 2752
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; Sequence 173, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: 1..4029
; LOCATION: /note="preliminary sequence for
; OTHER INFORMATION: human TRT CDNA insert of
; OTHER INFORMATION: plasmid pGRN121"
; US-08-854-050-173
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Query Match 95.7%; Score 3832.6; DB 4; Length 4029;

Best Local Similarity 97.9%; Pred. No. 1.6e-226;			
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QY	188	GGACCCGGCGCTTCCGCGCGCTGCTGCGCCAGTGCCTGCTGCTGAAGAGAGCTGTGCG	247
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QY	248	ACG	307
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QY	308	CCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	367
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QY	488	CCGCGTGGCGACGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	547
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QY	668	CTGGAACATAGCGTCAAGGAGCGCGGGTCCCTGCGGCTGCGAGCCCGCGGGTGGAG	727
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QY 1088 GCCCTCTCTCTACTC-AGCTCTGTAGAGCCCCAGCTGACTGGCGCTC-GGAGGCTCGTG 1145
Db 1075 NCCCTCTCTCTACTCAATATATGTAGAGCCAGCTGACTGGCTTCGGAGGTTGCTG 1134
QY 1146 GAGACCATCTTCTGTGGTTCAGAGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGC 1205
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Db 3953 GGGGAGTGTCTGTGGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4012
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RESULT 14
US-08-974-549A-4
: Sequence 4, Application US/08974549A
: Patent No. 6166178
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
: APPLICANT: Lingner, Joachim
: APPLICANT: Nakamura, Toru
: APPLICANT: Chapman, Karen B.
: APPLICANT: Morin, Gregg B.
: APPLICANT: Harley, Calvin B.
: APPLICANT: Andrews, William H.
: TITLE OF INVENTION: Human Telomerase Catalytic Subunit
: NUMBER OF SEQUENCES: 727
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/974,549A
: FILING DATE: 19-NOV-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/724,643
: FILING DATE: 01-OCT-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/844,419
: FILING DATE: 18-APR-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/846,017
: FILING DATE: 25-APR-1997
: PRIOR APPLICATION DATA:

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1 APPLICATION NUMBER: US 08/851,843
2 FILING DATE: 06-MAY-1997
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US 08/854,050
5 FILING DATE: 09-MAY-1997
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 08/911,312
8 FILING DATE: 14-AUG-1997
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 08/912,951
11 FILING DATE: 14-AUG-1997
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 08/915,503
14 FILING DATE: 14-AUG-1997
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: WO PCT/US97/17618
17 FILING DATE: 01-OCT-1997
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: WO PCT/US97/17885
20 FILING DATE: 01-OCT-1997
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Apple, Randolph Ted
23 REGISTRATION NUMBER: 36,429
24 REFERENCE/DOCKET NUMBER: 015389-002610US
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (415) 576-0200
27 TELEFAX: (415) 576-0300
28 INFORMATION FOR SEQ ID NO: 4:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 3855 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: cDNA
35 FEATURE:
36 NAME/KEY: -
37 LOCATION: 1..3855
38 OTHER INFORMATION: /note="nucleic acid sequence with an
39 OTHER INFORMATION: open reading frame encoding a delta-182
40 OTHER INFORMATION: variant polypeptide"
41 FEATURE:
42 NAME/KEY: CDS
43 LOCATION: 56..2479
44 OTHER INFORMATION: /product="delta-182 variant
45 OTHER INFORMATION: polypeptide"
46 US-08-974-549A-4

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Query Match	94.8%;	Score 3797;	DB 4;	Length 3855;
Best Local Similarity	94.68;	Pred. No. 2.3e-224;		
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			Indels	218;
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RESULT 15
US-08-974-549A-721
; Sequence 721, Application US/08974549A
; Patent No. 6166178
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

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? APPLICATION NUMBER: US 08/854,050
? FILING DATE: 09-MAY-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/911,312
? FILING DATE: 14-AUG-1997
? PRIOR APPLICATION DATA:
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? APPLICATION NUMBER: US 08/915,503
? FILING DATE: 14-AUG-1997
? PRIOR APPLICATION DATA:
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? FILING DATE: 01-OCT-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/US97/17885
? FILING DATE: 01-OCT-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Apple, Randolph Ted
? REGISTRATION NUMBER: 36,429
? REFERENCE/DOCKET NUMBER: 015389-002610US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 721:
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US-08-974-549A-721

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Search completed: April 17, 2003, 02:09:06
Job time : 180 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2003, 14:48:19 ; Search time 10138 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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4	3982.6	99.4	4037	6	E36819	E36819 Human telom
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6	3969	99.1	4015	6	AR104587	AR104587 Sequence
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ACCESSION	AX001446				
VERSION	AX001446.1	GI:7241612			
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ORGANISM	unclassified.				
REFERENCE	1. (bases 1 to 4042)				
AUTHORS	Wick, M. and Hagen, G.				
TITLE	HUMAN CATALYTIC TELOMERASE SUB-UNIT AND ITS DIAGNOSTIC AND THERAPEUTIC USE				
JOURNAL	Patent: WO 9859040-A 1 30-DEC-1998;				

FEATURES WICK MARESA (DE); BAYER AG (DE)
Location/Qualifiers
source 1. 4042
/organism="unidentified"
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BASE COUNT 684 a 1364 c 1277 g 717 t
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Query Match 99.8%; Score 3996; DB 6; Length 4042;
Best Local Similarity 99.1%; Pred. No. 2e-93;
Matches 4006; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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DEFINITION Sequence 2 from Patent WO9933998.
ACCESSION AX003121
VERSION AX003121.1 GI:9926983

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REFERENCE	1 (bases 1 to 4042)
AUTHORS	Wick, M. and Hagen, G.
TITLE	Regulatory dna sequences of the human catalytic telomerase sub-unit gene, diagnostic and therapeutic use thereof
JOURNAL	Patent: WO 9933998-A 2.08-JUL-1999;
FEATURES	WICK MARESA (DE); BAYER AG (DE)
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QY	901	AAGAAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCACGCCACATCCACCCATCCGTGG	960
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QY	961	GCCGCCAGACACACGCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGC	1020
Db	961	GCCGCCAGACACACGCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGC	1020
QY	1021	CTTGTCCCCCGGGTAGCGCCGAGACCAAGCACCTTCTCTACTCTCAGGCGACAAGAGC	1080
Db	1021	CTTGTCCCCCGGGTAGCGCCGAGACCAAGCACCTTCTCTACTCTCAGGCGACAAGAGC	1080
QY	1081	AGCTGCGGGCCCTCTCTCTACTCAGCTCTCTGAGGGCCAGCCTGACTGGCGCTCGAGGC	1140
Db	1081	AGCTGCGGGCCCTCTCTCTACTCAGCTCTCTGAGGGCCAGCCTGACTGGCGCTCGAGGC	1140
QY	1141	TCGTGGAGACCATCTTCTTGCGGTCCAGGCCCCGTGATGCCAGGGACTCCCCGACAGTTGC	1200
Db	1141	TCGTGGAGACCATCTTCTTGCGGTCCAGGCCCCGTGATGCCAGGGACTCCCCGACAGTTGC	1200
QY	1201	CCCGCCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTGAGAGCTTGGAAC	1260
Db	1201	CCCGCCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTGAGAGCTTGGAAC	1260
QY	1261	ACGGCGAGTGCCCTACGGGGTGCTCCTCAGAGCGCACTGCCCCGCTGCGAGCTGCGTCA	1320
Db	1261	ACGGCGAGTGCCCTACGGGGTGCTCCTCAGAGCGCACTGCCCCGCTGCGAGCTGCGTCA	1320
QY	1321	CCCCAGCAGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCGAGG	1380
Db	1321	CCCCAGCAGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCGAGG	1380
QY	1381	AGGAGGACACAGACCCCCCGTGCCTGGTGACAGTGTCTCCGCCACAGACAGACGCCCTGGC	1440
Db	1381	AGGAGGACACAGACCCCCCGTGCCTGGTGACAGTGTCTCCGCCACAGACAGACGCCCTGGC	1440
QY	1441	AGGTGTACGGCTTCTGTGCGGCGCTGCCCTGCGCGCGGCTGTGCCCCAGGCTCTGGGGCT	1500
Db	1441	AGGTGTACGGCTTCTGTGCGGCGCTGCCCTGCGCGCGGCTGTGCCCCAGGCTCTGGGGCT	1500
QY	1501	CCAGGCACAACGAACGCCGCTTCCCTCAGGAACACCAAGATTCTATCTCCCTGGGGAAGC	1560
Db	1501	CCAGGCACAACGAACGCCGCTTCCCTCAGGAACACCAAGATTCTATCTCCCTGGGGAAGC	1560
QY	1561	ATGCCAAGCTCTCGCTGCAGAGACTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGC	1620
Db	1561	ATGCCAAGCTCTCGCTGCAGAGACTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGC	1620
QY	1621	TGCGCAGGAGCCCGAGGGGTGGCTGTGTTCCGGCCGACAGAGCACCGTCTGCGTGAGGAGA	1680
Db	1621	TGCGCAGGAGCCCGAGGGGTGGCTGTGTTCCGGCCGACAGAGCACCGTCTGCGTGAGGAGA	1680
QY	1681	TCCTGGCCAAAGTTCTCTGCACCTGCGCTGATGAGTGTGTACTGTCTGAGCTGCTCAGGTTT	1740
Db	1681	TCCTGGCCAAAGTTCTCTGCACCTGCGCTGATGAGTGTGTACTGTCTGAGCTGCTCAGGTTT	1740
QY	1741	TCCTTTATGTACCGGAGACACAGTTTCAAAGAACAGGCTTTTTCTACCGGAAGAGTG	1800
Db	1741	TCCTTTATGTACCGGAGACACAGTTTCAAAGAACAGGCTTTTTCTACCGGAAGAGTG	1800
QY	1801	TCCTGAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACCTTGAAGAGGGTGCAGCTGCGGG	1860
Db	1801	TCCTGAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACCTTGAAGAGGGTGCAGCTGCGGG	1860

Db 4021 AAAAAAAAAAAAAAAAAAAAAA 4042

RESULT 3				
BD011070				
LOCUS	BD011070	4037 bp	DNA	
DEFINITION	Human telomerase catalytic subunit.		linear	PAT 31-JAN-2002
ACCESSION	BD011070			
VERSION	BD011070.1	GI:18639443		
KEYWORDS	JP 2001081042-A/27.			
SOURCE	unidentified.			
ORGANISM	unidentified.			
REFERENCE	unclassified.			
AUTHORS	1 (bases 1 to 4037)			
TITLE	Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,			
JOURNAL	Harley,C.B. and Andrews,W.H.			
	Human telomerase catalytic subunit			
	Patent: JP 2001081042-A 27 27-MAR-2001;			
	GERON CORP.,UNIVERSITY TECHNOLOGY CORP			
COMMENT	OS Unidentified			

BASE COUNT	ORIGIN				
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					4
					others

Query Match	99.48;	Score 3982.6;	DB 6;	Length 4037;
Best Local Similarity	98.98;	Pred. No. 4.3e-93;		
Matches 3992;	Conservative			

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Db	1	GCAGCGCTGCCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGGCCACCCCCCGCATGCC	67
QY	68	CGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT	127
Db	61	CGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT	127
QY	128	GCCGCTGGCCACGTTCTGTCGGCGCCCTGGGGCCCCCAGGCGCTGCGCGCTGTCAGCGCGG	187
Db	121	GCCGCTGGCCACGTTCTGTCGGCGCCCTGGGGCCCCCAGGCGCTGCGCGCTGTCAGCGCGG	187
QY	188	GGACCCGCGCGGCTTTCCGCGCGCTGTGTCGCCAGTGCCTGCTGTCGCTCCCTGGGACGC	247
Db	181	GGACCCGCGCGGCTTTCCGCGCGCTGTGTCGCCAGTGCCTGCTGTCGCTCCCTGGGACGC	247
QY	248	ACGGCGCGCCCCCGCGCCCTCTCCGCCAGGTGTCCTGCGTGAAGAGACTGTGGC	307
Db	241	ACGGCGCGCCCCCGCGCCCTCTCCGCCAGGTGTCCTGCGTGAAGAGACTGTGGC	307
QY	308	CCGAGTGTGACAGAGGCTGTGCGAAGCGCGCGCGCAGAAAGTGTGCTGGCCTTCGGCTTCGC	367

[illegible]

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1441 CGGCTTCGTTGCGGGGCTGCTGCTGCGCCGGGCTGTGTCGCCCCAGGCTCTGTGGGGCTCCAGGCA 1500
QY 1508 CAACGAACGCCGCTTCTCAGAGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGCCAA 1567
1501 CAACGAACGCCGCTTCTCAGAGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGCCAA 1560
QY 1568 GCTCTCGCTGAGAGAGCTGACGTGAGAGAGATGAGCGTGGGGACTGGCTTGGCTGGCGAG 1627
1561 GCTCTCGCTGAGAGAGCTGACGTGAGAGAGATGAGCGTGGGGACTGGCTTGGCTGGCGAG 1620
QY 1628 GAGCCCAAGGGGTTGGCTGTGTCGCCCGCGAGACACCGCTCTGCTGAGAGATCCTGGC 1687
1621 GAGCCCAAGGGGTTGGCTGTGTCGCCCGCGAGACACCGCTCTGCTGAGAGATCCTGGC 1680
QY 1688 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGCTGAGCTGCTCAAGGCTCTTCTTTA 1747
1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAAGGCTCTTCTTTA 1740
QY 1748 TGTACAGGAGACACAGTTTCAAAAGAACAGAGCTTTTCTAACCGGAAGTGTCTGGAG 1807
1741 TGTACAGGAGACACAGTTTCAAAAGAACAGAGCTTTTCTAACCGCGCAAGTGTCTGGAG 1800
QY 1808 CAAGTTCAAAGCATTTGAATCAGACAGACACTTGAAGAGGGTGCAGCTGGGAGCTGTC 1867
1801 CAAGTTCAAAGCATTTGAATCAGACAGACACTTGAAGAGGGTGCAGCTGGGAGCTGTC 1860
Db 1868 GGAAGCAGAGGTCAGGCGAGCATGCGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1927
1861 GGAAGCAGAGGTCAGGCGAGCATGCGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1920
QY 1928 CTTCATCCCCAAGCCTGACAGGGGCTGCGCGCATTTGTGAACATGACTACGTCTGGGAGC 1987
1921 CTTCATCCCCAAGCCTGACAGGGGCTGCGCGCATTTGTGAACATGACTACGTCTGGGAGC 1980
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QY 2732 GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTGTACAGAT 2791
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QY 2792 GCCGGCCACAGGCTATTCCTGCTGCTGGGCTGCTGATACCCGAGCCCTGAGGT 2851
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QY 3272 GACTCGACACCGTGTACCTACGTGCGCACTCTGGGTTCACTCAGACAGCCAGAGCGA 3331
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QY 3332 GCTGAGTGGAAAGCTCCCGGGGACGAGCTGACTGCCCTGGAAGGCCGAGCCAAACCCGCG 3391
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QY 3572 CATGTCGGGCTGAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGGCCAAGGCT 3631
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Db 3661 GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCTCACCAGGAGCGCGCTTCCACTCCACATAGGAATAGTCATCC 3751
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Db 3721 GGGCCAGCTTTTCTCACCAGGAGCGCGCTTCCACTCCACATAGGAATAGTCATCC 3780
QY 3752 CCAGATTGCGCATTTGTCACCCCTGCGCTGCGCTTTCCTTGCCTTCCACCCCGCATCC 3811
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E36819 4037 bp DNA linear PAT 18-JUN-2001
LOCUS Human telomerase catalytic subunit promoter.
DEFINITION E36819
ACCESSION E36819
VERSION E36819.1 GI:13022782
KEYWORDS JP 1999253177-A/27.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 4037)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 27 21-SEP-1999;
JERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 1999253177-A/27
PD 21-SEP-1999
PE 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724.643,18-APR-1997 US 08/844.419, PR
25-APR-1997 US 08/846.017,06-MAY-1997 US 08/851.843, PR
09-MAY-1997 US 08/854.050,14-AUG-1997 US 08/911.312, PR
14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/915.503 PI THOMAS
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HAREI,WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
PC C12Q1/02,
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
Strandedness: Single;
CC Topology: linear;
FH Key Location/Qualifiers
FT CDS 56..3454.
Location/Qualifiers

FEATURES

Location/Qualifiers
56..3454.
CDS

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Query Match 99.4%; Score 3982.6; DB 6; Length 4037;
Best Local Similarity 98.9%; Pred. No. 4.3e-93;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCGTCTGCTGCGCACAGTGGGAAGCCCTGCGCCCGCCACCCCGCGATGCC 67
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Db 1 GCAGCGCTGCGTCTGCTGCGCACAGTGGGAAGCCCTGCGCCCGCCACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 127
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Db 61 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 120
QY 128 GCGCGCTGCGCAGTTCGTGCGGCGCCTGCGGCGCCAGAGGCTGGCGGCTGCTGCAAGCGCG 187
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Db 241 ACG 300
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QY	1028	CCCGETAACGCCGAGACCAAGCATTCTCTACTCTCTACGGGACACAAGGAGTGGC	1087
Db	1021	CCCGETAACGCCGAGACCAAGCATTCTCTACTCTCTACGGGACACAAGGAGTGGC	1080
QY	1088	GCCCTCCTTCTACTACAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGSAGGCTTGGA	1147
Db	1081	GCCCTCCTTCTACTACAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGSAGGCTTGGA	1140
QY	1148	GACCATCTTTCTGGGTTCCAGAGCCCTTGATGCCAGGSACTCCCGCAGGTTGCCGCT	1207
Db	1141	GACCATCTTTCTGGGTTCCAGAGCCCTTGATGCCAGGSACTCCCGCAGGTTGCCGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAAATGGCGCCCTGTCTTGAGACTGCTTGGGAACACGCGCA	1267
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QY	1268	GTGCCCCAAGGGGTGCTCTCAAGACGCACTGCCGCTCGGCGGCCCCGAGGAGAGA	1327
Db	1261	GTGCCCCAAGGGGTGCTCTCAAGACGCACTGCCGCTCGGCGGCCCCGAGGAGAGA	1320
QY	1328	AGCCGGTGTCTGTGCCCCGGGAGAGGCCCGAGGCTCTGTGGCGGCCCGAGGAGAGA	1387
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QY	1388	CACAGACCCCCGTGCTGTGAGTGCAGTGTCTCCGACACACAGCACAGCCCTGGACGTGA	1447
Db	1381	CACAGACCCCCGTGCTGTGAGTGCAGTGTCTCCGACACACAGCACAGCCCTGGACGTGA	1440
QY	1448	CGGCTTCGTGCGGGCTGCCCTGGCGCGGCTGTGTCGCCCCAGGCTCTGGGGCTCCAGGA	1507
Db	1441	CGGCTTCGTGCGGGCTGCCCTGGCGCGGCTGTGTCGCCCCAGGCTCTGGGGCTCCAGGA	1500
QY	1508	CAACGAACGCCGCTTCTCAGGAACCAAGAGTTCACTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCCGCTTCTCAGGAACCAAGAGTTCACTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTGCTGACAGAGCTGACGTGGAAGTAGAGCTGGCGGACTGCCCTTGGCTGCGCAG	1627
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QY	1628	GAGCCCAAGGGGTGGCTGTGTCCGGCGGACAGAGCACCGTCTGCGTAGAGATCTGGC	1687
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Db	1681	CAAGTTCCTGACACTGGCTGATAGTGTGTAAGTGTGAGCTGAGCTCAGGCTCTTTCTTA	1740
QY	1748	TGTCACGGAGACCAAGTTTCAAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTGAG	1807
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QY	1808	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAAGGGTGAAGTCCGGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAAGGGTGAAGTCCGGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTGACAGGACATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1927
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QY	1928	CTTCATCCCCAAGCTGACGGGCTGCGGCCGATTTGTGACATGAGACTACGTGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCTGACGGGCTGCGGCCGATTTGTGACATGAGACTACGTGTGGAGC	1980
QY	1988	CAGAACGTTCCGACAGAAAAAGGGCCGAGCGTCTACCTGAGAGGTGAAGCACTGTT	2047
Db	1981	CAGAACGTTCCGACAGAAAAAGGGCCGAGCGTCTACCTGAGAGGTGAAGCACTGTT	2040

QY	2048	CAGCGTGCCTCACTACGAGCGGGCGCGCCCGCCCTCTCTGGCGCCTCTGTGGG	2107
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Db	2101	CCTGACGATATCCACAGAGGCGCTGGCGCACCTTCCTGCTGCTGCTGTGCGGGCCAGAACCC	2160
QY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCTGAGCTGTA-----CATCCCCA	2220
QY	2192	GGACAGGCTTCACGAGGCTCATTCGCCAGCATCATCAAAACCCAGAACAGCTACTGCGTGG	2251
Db	2221	GGACAGGCTTCACGAGGCTCATTCGCCAGCATCATCAAAACCCAGAACAGCTACTGCGTGG	2280
QY	2252	TCGGTATGCCGTGGTCCAGAGAGCGCCCATGGGACAGCTCCCGCAAGGCGCTTCAAGAGCCA	2311
Db	2281	TCGGTATGCCGTGGTCCAGAGAGCGCCCATGGGACAGCTCCCGCAAGGCGCTTCAAGAGCCA	2340
QY	2312	CGTCTCTACCTTCACAGAGAGCTCCAGCCGTACATTCGAGAGTTCGTGGCTCACCTGCAGGA	2371
Db	2341	CGTCTCTACCTTCACAGAGAGCTCCAGCCGTACATTCGAGAGTTCGTGGCTCACCTGCAGGA	2400
QY	2372	GACCAAGCCCGCTGAGAGGATGCCGTCTCATCGACAGAGAGCTCTCCCTGAATGAGGCCAG	2431
Db	2401	GACCAAGCCCGCTGAGAGGATGCCGTCTCATCGACAGAGAGCTCTCCCTGAATGAGGCCAG	2460
QY	2432	CAGTGGCTCTTCGACAGCTCTTCCTACGCTTCATATGACCACCAAGCCGTCGATCAAGGG	2491
Db	2461	CAGTGGCTCTTCGACAGCTCTTCCTACGCTTCATATGACCACCAAGCCGTCGATCAAGGG	2520
QY	2492	CAGTCTCTACCTCCAGTGCACAGGGATCCCGCAGGCGCTCCATCTCTCCACAGCTGCTCTG	2551
Db	2521	CAGTCTCTACCTCCAGTGCACAGGGATCCCGCAGGCGCTCCATCTCTCCACAGCTGCTCTG	2580
QY	2552	CAGCCTGTGCTACGCGGCACATGAGAACAAAGCTGTTTCGGGGATTCGGCGGGACGGGCT	2611
Db	2581	CAGCCTGTGCTACGCGGCACATGAGAACAAAGCTGTTTCGGGGATTCGGCGGGACGGGCT	2640
QY	2612	GCTCCGCGTGTGGTGAATGATTTCTTGTGTGACACTCACCTCACCGCGAAGAAC	2671
Db	2641	GCTCCGCGTGTGGTGAATGATTTCTTGTGTGACACTCACCTCACCGCGAAGAAC	2700
QY	2672	CTTCCTCAGAGACCTGTGTCGAGGTGTCCTGAGTATGCTGCGTGGTGAACCTTCGCGAA	2731
Db	2701	CTTCCTCAGAGACCTGTGTCGAGGTGTCCTGAGTATGCTGCGTGGTGAACCTTCGCGAA	2760
QY	2732	GACAGTGGGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTGTTCAGAT	2791
Db	2761	GACAGTGGGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTGTTCAGAT	2820
QY	2792	GCGCGCCACAGCGCCTATTCCTCCGTGGCTGCGCCTGCTGATATCCCGAGCCCTGAGAGT	2851
Db	2821	GCGCGCCACAGCGCCTATTCCTCCGTGGCTGCGCCTGCTGATATCCCGAGCCCTGAGAGT	2880
QY	2852	GCAGAGCGACTACTCCAGCTATGCGCGAGCCCTCCATCAGAGCCAGTGTACCTTCAACCG	2911
Db	2881	GCAGAGCGACTACTCCAGCTATGCGCGAGCCCTCCATCAGAGCCAGTGTACCTTCAACCG	2940
QY	2912	CGGCTTCAAGGCTGGGAGAGAACATGCGTGCAGAACTCTTTGGGGCTCTTGGCGCTGAAGT	2971
Db	2941	CGGCTTCAAGGCTGGGAGAGAACATGCGTGCAGAACTCTTTGGGGCTCTTGGCGCTGAAGT	3000
QY	2972	TCACAGCGCTGTTCTGGAATTCAGGTGAACAGAGCTCCAGAGCGGTGTCACCAACATCTA	3031
Db	3001	TCACAGCGCTGTTCTGGAATTCAGGTGAACAGAGCTCCAGAGCGGTGTCACCAACATCTA	3060
QY	3032	CAGATCTCTCTGCTGACAGCGGTACAGGTTTCAGGCATGTTGCTGACAGCTCCCATTTCA	3091
Db	3061	CAGATCTCTCTGCTGACAGCGGTACAGGTTTCAGGCATGTTGCTGACAGCTCCCATTTCA	3120
QY	3092	TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGCGCTCCCT	3151

RESULT 5	AX391846	AX391846	4070 bp	DNA	Linear	PAT 23-MAR-2002
LOCUS	AX391846					
DEFINITION	Sequence 1	from Patent WO0216555.				
ACCESSION	AX391846					
VERSION	AX391846.1	GI:19700428				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					

[illegible]

Db 799 GCTGCCCCTAGACCCGGAGCGGACGCCCGTTGGGCAGGGGTCTCTGGGCCACCCGGGCAGG 858
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Db 859 ACGCTGGACCGAGTAGCCGTGTTTCTGTGTGTGTCACTGCGACACCCGCCGAAGAA 918
QY 906 GCCACCTCTTTGGAGGGGTGGGCTCTGTGGCACGGCCACTTCCACCATTCCGTTGGGCCGC 965
Db 919 GCCACCTCTTTGGAGGGGTGGGCTCTGTGGCACGGCCACTTCCACCATTCCGTTGGGCCGC 978
QY 966 CAGCACACGCGGGGCCCCCATCCACATCGCGGCCACCCACGTCCTGGGACACGCTTGT 1025
Db 979 CAGCACACGCGGGGCCCCCATCCACATCGCGGCCACCCACGTCCTGGGACACGCTTGT 1038
QY 1026 CCCCCGTTGACGCCGAGACCAAGCACCTTCTACTCTCTCAGCGGACAGAGAGAGAGCTG 1085
Db 1039 CCCCCGTTGACGCCGAGACCAAGCACCTTCTACTCTCTCAGCGGACAGAGAGAGAGCTG 1098
QY 1086 CGGCCCTCTCTCTACTACTAGCTCTCTGAGGCCACGCTGACTGGGCTCGGAGGCTCGTG 1145
Db 1099 CGGCCCTCTCTCTACTACTAGCTCTCTGAGGCCACGCTGACTGGGCTCGGAGGCTCGTG 1158
QY 1146 GAGACCATCTTCTGGGTTCAGGSCCTGATGCCAGGAGCTCCCGCAGGTTGCCCGC 1205
Db 1159 GAGACCATCTTCTGGGTTCAGGSCCTGATGCCAGGAGCTCCCGCAGGTTGCCCGC 1218
QY 1206 CTGCCCCAGCGCTACTGGAATGCGGCCCCCTGTTCTGAGCTGCTTGGGAACACGCG 1265
Db 1219 CTGCCCCAGCGCTACTGGAATGCGGCCCCCTGTTCTGAGCTGCTTGGGAACACGCG 1278
QY 1266 CAGTGCCCTACGGGGTGTCTCTCAAGACGACACTGCCCCGCTGGAGGCTGGTCAACCCA 1325
Db 1279 CAGTGCCCTACGGGGTGTCTCTCAAGACGACACTGCCCCGCTGGAGGCTGGTCAACCCA 1338
QY 1326 GCAGCCGGTGTCTGTGCCCCGGGAGAAAGCCGCTGTGTGGGGCCCCCGAGAGAGAG 1385
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QY 1386 GACACAGACCCCGTCTGCTGTGTGAGCTGCTCCGCGACACAGACGCCCTGTGCAGGTG 1445
Db 1399 GACACAGACCCCGTCTGCTGTGTGAGCTGCTCCGCGACACAGACGCCCTGTGCAGGTG 1458
QY 1446 TACGGCTTCTGTGGGGGCGCTGCGCCGCTGTGTGCCCCAGGCTCTGGGGCTCCAG 1505
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QY 1506 CACAACGAACGCGCTTCTCAGGAACCAACGAAGTTCACTCTCTGGGGAAGCATGCC 1565
Db 1519 CACAACGAACGCGCTTCTCAGGAACCAACGAAGTTCACTCTCTGGGGAAGCATGCC 1578
QY 1566 AAGCTCTGCTGACGAGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCC 1625
Db 1579 AAGCTCTGCTGACGAGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCC 1638
QY 1626 AGGAGCCCCAGGGGTTGGCTGTTCGCGCGCAGAGCACCGTGTGCTGAGAGATCTG 1685
Db 1639 AGGAGCCCCAGGGGTTGGCTGTTCGCGCGCAGAGCACCGTGTGCTGAGAGATCTG 1698
QY 1686 GCCAAGTCTGCACTGGCTGATGAGTGTGACGTGCTGAGAGCTGCTCAGGCTTTCTTT 1745
Db 1699 GCCAAGTCTGCACTGGCTGATGAGTGTGACGTGCTGAGAGCTGCTCAGGCTTTCTTT 1758
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Db 1819 AGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACCTGAAGAGGCTGAGGAGCTG 1878
QY 1866 TCGGAAGCAGAGGTGAGGACAGCATCGGGAAGCCAGGCCGCTGCTGACGTCCAGACTC 1925
Db 1879 TCGGAAGCAGAGGTGAGGACAGCATCGGGAAGCCAGGCCGCTGCTGACGTCCAGACTC 1938

QY 1926 CGCTTCAATCCCAAGCTGACGGGCTGGCGGCCGATTTGTGAACATGAGCTACGTCTGGGA 1985
Db 1939 CGCTTCAATCCCAAGCTGACGGGCTGGCGGCCGATTTGTGAACATGAGCTACGTCTGGGA 1998
QY 1986 GCCAGAAGCTTCCGAGAGAAAGAGGGCCGAGCGTCTCACCCTCGAGGCTGAAGCACTG 2045
Db 1999 GCCAGAAGCTTCCGAGAGAAAGAGGGCCGAGCGTCTCACCCTCGAGGCTGAAGCACTG 2058
QY 2046 TTACGCGTCTCAACTPACGAGCGGGCGCGGCCCTCTGAGGCGCTCTGTGCTG 2105
Db 2059 TTACGCGTCTCAACTPACGAGCGGGCGCGGCCCTCTGAGGCGCTCTGTGCTG 2118
QY 2106 GGCTGGACGATATCCACAGGGGCTGGCGACCTTCTGCTGCTGTGGGCCACAGGAC 2165
Db 2119 GGCTGGACGATATCCACAGGGGCTGGCGACCTTCTGCTGCTGTGGGCCACAGGAC 2178
QY 2166 CCGCGCTGAGCTGTA-----CAVCCC 2189
Db 2179 CCGCGCTGAGCTGTA-----CAVCCC 2238
QY 2190 CAGGACAGGCTCAGGAGGTGATCGCCAGCATATCAAAACCCAGAAACAGTACTGCGTG 2249
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QY 2250 CGTGGTATCCCGTGTGTCCAGAGGGCCGCCCATGGGCAAGTCCGCAAGGCTTCAAGAGC 2309
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QY 2310 CAGCTCTCTACCTTGACAGACCTCCAGCCGCTACATGCCACAGTTCGTGGCTCACCTGCGAG 2369
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QY 2370 GAGACAGCCCGCTGAGGAGATGCCGTCGTATCGAGAGAGCTCTCTCTGAATGAGGCC 2429
Db 2419 GAGACAGCCCGCTGAGGAGATGCCGTCGTATCGAGAGAGCTCTCTCTGAATGAGGCC 2478
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Db 2479 AGCAGTGGCCTCTTCGACGCTTCTCTACGCTTCAATGTGCCAACACGCGTGGCATCAGG 2538
QY 2490 GGCAAGTCTTACGTTGAGTGGCAAGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTC 2549
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QY 2550 TGCAGCCTGTGTACGCGGACATGAGAAACAAGCTTTTGGGGGATTCGGCGGACGGG 2609
Db 2599 TGCAGCCTGTGTACGCGGACATGAGAAACAAGCTTTTGGGGGATTCGGCGGACGGG 2658
QY 2610 CTGCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAA 2669
Db 2659 CTGCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAA 2718
QY 2670 -ACCTTCTCAGACCCCTGGTCCGAGGTGCCCTGAGTATGCTGCTGGTGTGACTTGGG 2729
Db 2719 ACCTTCTCAGACCCCTGGTCCGAGGTGCCCTGAGTATGCTGCTGGTGTGACTTGGG 2778
QY 2730 AAGACAGTGTGAACCTTCCGTAGAGAGAGAGCCCTGGGTGGACGCGCTTTGTTACG 2789
Db 2779 AAGACAGTGTGAACCTTCCGTAGAGAGAGAGCCCTGGGTGGACGCGCTTTGTTACG 2838
QY 2790 ATGCGGGCCACGGCCTATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2849
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QY 2850 GTGCAGAGGACTACTACAGCTATGCCCCGAGCTTCATCAGAGCCAGTCTCACCTTCAAC 2909
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QY 2910 CCGGCGCTTCAAGGCTGGGAAGACATGCTGCAAACTCTTTGGGCTCTTGGCGCTGAAG 2969
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RESULT 6	ARI04587	LOCUS	ARI04587	Sequence 224	from patent US 6093809.	4015 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION									

[illegible]

		mismatches	U	Indels	36	Gaps
QY	8	GCAGCGCTGCGTCTGTGCGGCACAGTGGAGAGCCCTGGCCCCGGCCACACCCCGGATGCC	67			
Db	1	GCAGCGCTGCGTCTGTGCGGCACAGTGGAGAGCCCTGGCCCCGGCCACACCCCGGATGCC	67			
QY	68	GCAGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT	127			
Db	61	GCAGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT	120			
QY	128	GCCGCTGGCCACGTTCTGTGCGGCGCCCTGGGGCCCCCAGGCGCTGGCGGTGTGCAGCGCG	187			
Db	121	GCCGCTGGCCACGTTCTGTGCGGCGCCCTGGGGCCCCCAGGCGCTGGCGGTGTGCAGCGCG	180			
QY	188	GGACCCCGGCGCTTTCGCGCGCTGTGCGCCAGTGCCTGTGTGCGTCCCTGGAGCG	247			
Db	181	GGACCCCGGCGCTTTCGCGCGCTGTGCGCCAGTGCCTGTGTGCGTCCCTGGAGCG	240			
QY	248	ACGCGCCGCCCCCGCCGCCCTCTCCGCGCAGGTGTCTGCTGAAGAGCTGTGCG	307			
Db	241	ACGCGCCGCCCCCGCCGCCCTCTCCGCGCAGGTGTCTGCTGAAGAGCTGTGCG	300			
QY	308	CCGAGTCTGACAGAGCTGTGCGAGCGCGCGCGGCGAAGAACGTGCGCTTGGCGTTCGC	367			
Db	301	CCGAGTCTGACAGAGCTGTGCGAGCGCGCGGCGAAGAACGTGCGCTTGGCGTTCGC	360			
QY	368	GCTGCTGGACGGGGGCGGGGCCCCCGAGGCGCTTCAACCAACAGCGTGGCAGCTA	427			
Db	361	GCTGCTGGACGGGGGCGGGGCCCCCGAGGCGCTTCAACCAACAGCGTGGCAGCTA	420			
QY	428	CCTGCCCAACACGCTGACCGGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGTGCG	487			
Db	421	CCTGCCCAACACGCTGACCGGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGTGCG	480			
QY	488	CCGCGTGGCGACGAGCTGCTGCTTCACTGCTGCGACGCTGCGCGCTTTGTGTGCTGT	547			
Db	481	CCGCGTGGCGACGAGCTGCTGCTTCACTGCTGCGACGCTGCGCGCTTTGTGTGCTGT	540			
QY	548	GGCTCCACGCTGGCGCTACCAAGGTGTGCGGGCGCGCTGTACCAAGCTGGCGCTGCCAC	607			
Db	541	GGCTCCACGCTGGCGCTACCAAGGTGTGCGGGCGCGCTGTACCAAGCTGGCGCTGCCAC	600			
QY	608	TCAGGCGCGGGCCCCCGCCACACGCTAGTGAACCCGAAAGCGCTTGGGATGCGAAGCGGC	667			
Db	601	TCAGGCGCGGGCCCCCGCCACACGCTAGTGAACCCGAAAGCGCTTGGGATGCGAAGCGGC	660			
QY	668	CTGGAACCATAGCGTCAAGGAGCGCGGGGTCCCCCTGGGCTTGCAGCGCCCGGGTGGAG	727			
Db	661	CTGGAACCATAGCGTCAAGGAGCGCGGGGTCCCCCTGGGCTTGCAGCGCCCGGGTGGAG	720			
QY	728	GAGGCGGGGGCAGTGCACAGCGGAAGTCTGCGCTTGCCCAAGAGGCGCCAGCGTGGCGC	787			
Db	721	GAGGCGGGGGCAGTGCACAGCGGAAGTCTGCGCTTGCCCAAGAGGCGCCAGCGTGGCGC	780			
QY	788	TGCCCTGAGCCGGAGCGGAGCGCCGTTGGGCAAGGGGTCTTGCGGCCACCCGGGCAAGAC	847			

Db 781 TGCCCTGAGCGGAGCGGAGACGCCGTTGGGAGGGGTCTGGGCCACCCGGGAGAGAC 840
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Db 841 GCGTGGACCGAGTGAACCGTGGTTTCTGTGTGTCACCTGCCAGACCCGGCGAAGAAC 900
QY 908 CACCTCTTTGGAGGTTGCGCTCTTGCCACGCGCCACTGCCACCCATCCGTGGCCGCCA 967
Db 901 CACCTCTTTGGAGGTTGCGCTCTTGCCACGCGCCACTGCCACCCATCCGTGGCCGCCA 960
QY 968 GCACACGCGGGGCCCCCATTCACATCGCGGGCCACACGTCCTGGACACGCTTGTCC 1027
Db 961 GCACACGCGGGGCCCCCATTCACATCGCGGGCCACACGTCCTGGACACGCTTGTCC 1020
QY 1028 CCGGCTGTACGCCCGAGACCAACACTTCTCTACTCTCAGGCGACAAGAGACAGCTGCG 1087
Db 1021 CCGGCTGTACGCCCGAGACCAACACTTCTCTACTCTCAGGCGACAAGAGACAGCTGCG 1080
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QY 1328 AGCGGTGTCTGTGCCCCGGGAGAACCCAGGCTGTGTGGCGGCCCGAGAGAGAGA 1387
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QY 1388 CACAGACCCCGTCCCTGGTGTGAGCTGTCCGCCACAGACAGGCCCCCTGGCAGGTGTA 1447
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QY 1448 CGGCTTCGTGCGGGGCGCTGCGCGCGGTGTGCCCCAGGCTCTGGGGCTCCAGGCA 1507
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Db 1501 CAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTCAATCTCCCTGGGGAAGCATGCCAA 1560
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Db 1561 GCTTCGCTGACGAGAGCTGACGTGAAGATGACGCTGCGGGACTGCGCTTGCTGCCGAG 1620
QY 1628 GAGCCAGGGGTGGCTGTGTTCGGCGCAGAGACCGTCTGCGTGAAGATCTGGC 1687
Db 1621 GAGCCAGGGGTGGCTGTGTTCGGCGCAGAGACCGTCTGCGTGAAGATCTGGC 1680
QY 1688 CAAGTCTGACATGAGTGTGTAGTGTGACGTGCTGAGCTGCTCAGGTCTTTCTTTA 1747
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Db 1801 CAAGTTGCAAGCATTTGGAAATCAGACAGCACTTGAAGAGGTTGAGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGTCAAGGACATCGGGAAGCCAGGCCGCTGTGACGTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGTCAAGGACATCGGGAAGCCAGGCCGCTGTGACGTCCAGACTCCG 1920

Db 1861 GGAAGCAGAGTCAAGGACATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGACTCCG 1920
QY 1928 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGAGCTACTGTGGAGC 1987
Db 1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGAGCTACTGTGGAGC 1980
QY 1988 CAGAACGTTCCGACAGAAAAGAGGGCCGAGCGTCTACCTCGAAGGTGAAGGCACTGTT 2047
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Db 2581 CAGCCTGTGTACGGCGACATGAGAACAGCTGTTTGGCGGATTTGGCGGGAGCT 2640
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 Db 1081 GCCCTGCTTCTACTAGCTCTGTAGGCGCCAGCCTGACTGGCGCTGGAGGCTGTTGA 1140
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 Db 1441 CGGCTTCTGTGGGGGCGCTGCGCGCGCGGTGGCCCGAGGCTGTGGGCTCCAGGCA 1500
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RESULT 8
ARI82221

LOCUS ARI82221 4015 bp DNA Linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6337200.
ACCESSION ARI82221
VERSION ARI82221.1 GI:20225137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Morin,G.B.
TITLE Human telomerase catalytic subunit variants
JOURNAL Patent: US 6337200-A 1 08-JAN-2002;
FEATURES
source location/Qualifiers
BASE COUNT 663 a 1363 c 1275 g 714 t
ORIGIN

Query Match 99.1%; Score 3969; DB 6; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-93;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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DEFINITION Sequence 10 from Patent WO9940221.
ACCESSION AX019310
VERSION AX019310.1 GI:10043297
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 4015)
AUTHORS Dahm,M.W., Phelps,R.C. and Brockmeyer,C.
TITLE Method for quantitatively analyzing tumor cells in a body fluid and
test kits suited therefor
JOURNAL Patent: WO 9940221-A 10 12-AUG-1999;
DAHM MICHAEL W (DE); PHELPS ROBERT C (DE); BROCKMEYER CARSTEN (DE)
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BASE COUNT 663 a 1363 c 1275 g 714 t
ORIGIN
Query Match 99.1%; Score 3969; DB 6; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-93;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCTCTCTGCTGCGACGTGGGAAGCCTGCGCCCGCCACCCCGCGATGCC 67
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QY 128 GCGCGTGGCCACGTTCTGCGCGCGCGCTGGGCGCCAGGGCTGGCGGCTGGTGACGCGCG 187
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QY 188 GGAACCCCGCGGCTTTCGCGCGCGCTGCTGCGCGACGTGCTGTGCTGCGCTGCGCGACGC 247
Db 181 GGAACCCCGCGGCTTTCGCGCGCGCTGCTGCGCGACGTGCTGTGCTGCGCTGCGCGACGC 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCTCTTCCGCGCAGGTGTCTGCTGCGCGTGAAGAGCTGTGCG 307
Db 241 ACGGCGCGCGCGCGCGCGCGCGCTCTTCCGCGCAGGTGTCTGCTGCGCGTGAAGAGCTGTGCG 300
QY 308 CCGAGTGTGCAAGGCTGTGCGAGCGCGCGCGCGCGAAGACGTGTGCGCTTCCGCTGAGAGCTGTGCG 367
Db 301 CCGAGTGTGCAAGGCTGTGCGAGCGCGCGCGCGCGAAGACGTGTGCGCTTCCGCTTCCG 360
QY 368 GCTGTGAGAGGCGCGCGCGCGCGCGCGCGCGCGAGGCTTCAACCAACAGCGTGGCGAGCTA 427
Db 361 GCTGTGAGAGGCGCGCGCGCGCGCGCGCGCGCGAGGCTTCAACCAACAGCGTGGCGAGCTA 420
QY 428 CCTGCCCAACAGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGTGCG 487
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Db	3001	TCACACGCTG	TTTCTGATTTGCAAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3000
QY	3032	CAAGATTCCT	CTGCTGCAGCGCTACAGGTTTACCGCATGTGTGCTGCAGCTCCCATTTTCA	3031
Db	3061	CAAGATTCCT	CTGCTGCAGCGGTACAGGTTTACCGCATGTGTGCTGCAGCTCCCATTTTCA	3060
QY	3092	TCAGCAAGTT	TGGAAGAACCCACATTTTCTCCTGGCGGTATCTCTGACACGGCTCCCT	3120
Db	3121	TCAGCAAGTT	TGGAAGAACCCACATTTTCTCCTGGCGGTATCTCTGACACGGCTCCCT	3120
QY	3152	CTGCTACTCC	ATCCTGNAAGCCAGAACCGCAGGGATGTGCTGGGGGCCAAAGGGCGCCG	3180
Db	3181	CTGCTACTCC	ATCCTGNAAGCCAGAACCGCAGGGATGTGCTGGGGGCCAAAGGGCGCCG	3180
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QY	3272	GACTCGACAC	CGGTGTACACCTACGTGCCACTCTGGGGTCACTCAGGACAGCCAGACGCA	3300
Db	3301	GACTCGACAC	CGGTGTACACCTACGTGCCACTCTGGGGTCACTCAGGACAGCCAGACGCA	3300
QY	3332	GCTGAGTCGA	AGACTCCCGGGGACGACGCTGACTGCGCTGGAAGGCCGAGCCAAACCCGGC	3360
Db	3361	GCTGAGTCGA	AGACTCCCGGGGACGACGCTGACTGCGCTGGAAGGCCGAGCCAAACCCGGC	3360
QY	3392	ACTGCGCTCA	GACTTCAAGACCATCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA	3420
Db	3421	ACTGCGCTCA	GACTTCAAGACCATCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA	3420
QY	3452	GAGCAGACAC	CAGACGCCCTGTACGCGCGGCTTACGTCCAGGAGGAGGAGGGCGGCC	3480
Db	3481	GAGCAGACAC	CAGACGCCCTGTACGCGCGGCTTACGTCCAGGAGGAGGAGGGCGGCC	3480
QY	3512	CACACCCAG	CGCCGCAACCGCTGGAGTCTGAGGCTGAGTGAGTGTGCGCGAGGCCGTG	3540
Db	3541	CACACCCAG	CGCCGCAACCGCTGGAGTCTGAGGCTGAGTGAGTGTGCGCGAGGCCGTG	3540
QY	3572	CATGTCCGG	CTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGGCT	3600
Db	3601	CATGTCCGG	CTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGGCT	3600
QY	3632	GAGTGTCAAC	ACACCTGCGCTTCACTTCCCCACAGAGGCTGGCGCTCGCTCCACCCCA	3660
Db	3661	GAGTGTCAAC	ACACCTGCGCTTCACTTCCCCACAGAGGCTGGCGCTCGCTCCACCCCA	3660
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QY	3872	CCCTGTACAC	AGCGCAGACCCCTGCACCTGGATGGGGGTCCCTGTGGTCAAAATTGGGGG	3900
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DEFINITION AX133979          4015 bp          DNA          linear          PAT 15-MAY-2001
ACCESSION  AX133979
VERSION    AX133979.1  GI:14139919
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ORGANISM   human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            Chang,S.Y. and Santini,C.D.
            Quantitation of htert mrna expression
            Patent: EP 1108789-A 1 20-JUN-2001;
            F. HOFMANN-LA ROCHE AG (CH)
            location/Qualifiers
            1. .4015
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BASE COUNT 663 a      1363 c      1275 g      714 t
ORIGIN

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QY 68 GCGCGCTCCCGCTGCGCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT	127			
Db 61 GCGCGCTCCCGCTGCGCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT	120			
QY 128 GCGCGTGGCCACGTTGTTGCGCGCGCCCTGGGGCCCCAGGGCTGGCGGCTGTCAGCGCGG	187			
Db 121 GCGCGTGGCCACGTTGTTGCGCGCGCCCTGGGGCCCCAGGGCTGGCGGCTGTCAGCGCGG	180			
QY 188 GGAACCCGGCGGCTTCCGCGCGCTGTTGGCCAGTGCCTGTTGCGGTGCCCCTGGACGC	247			
Db 181 GGAACCCGGCGGCTTCCGCGCGCTGTTGGCCAGTGCCTGTTGCGGTGCCCCTGGACGC	240			
QY 248 ACGGCGGCCCCCGCCCCCTCTCTCCGCGCCAGGTGTCTGCTGAAGAGCTGTTGCC	307			
Db 241 ACGGCGGCCCCCGCCCCCTCTCTCCGCGCCAGGTGTCTGCTGAAGAGCTGTTGCC	300			
QY 308 CCGAGTGTGAGAGGGCTGTGCGAGCGCGCGCGGCGAAGACGTGCTGGCCTTGGCTTGGC	367			
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QY 368 GCTGCTGAGCGGGGCCCCGGGGGCCCCCGAGGCGCTTACCAACAGCGTGGCAGCTA	427			
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QY 428 CCTGCCAACACAGGTGACCGAGCCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCG	487			
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Db 481 CCGCGTGGGCGAGCAGCTGCTGTTCACTGCTGCGCACGCTGGCGGCTTGTGTGCTGT	540			
QY 548 GGTCCACAGCTGCGCTTACCAGGTGTGCGGGGCGCGCTGTACCAAGCTGGCGCTGCCAC	607			
Db 541 GGTCCACAGCTGCGCTTACCAGGTGTGCGGGGCGCGCTGTACCAAGCTGGCGCTGCCAC	600			
QY 608 TCAGGCGGCGGCCCCGCGCCACACAGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAAGGCGC	667			

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QY 668 CTGAACCATAGCGTTCAGGAGGAGCGGGGTCCCTGGGCTCCAGCCCGCGGTGGAG 727
Db 661 CTGGAACCATAGCGTTCAGGAGGAGCGGGGTCCCTGGGCTCCAGCCCGCGGTGGAG 720
QY 728 GAGGCGCGGGGGCAGTGGCCAGCGGAAGTCTGCCGTTGCCAAGAGGGCCAGCGTGGCG 787
Db 721 GAGGCGCGGGGGCAGTGGCCAGCGGAAGTCTGCCGTTGCCAAGAGGGCCAGCGTGGCG 780
QY 788 TGCCCCGTGAGCCGGAGCGGACCGCCGTTGGGCGAGGGGTCTGGGGCCACCCGGGCGAGGAC 847
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Db 841 GCGTGGACCGAGTGAACCGTGGTTTCTGTGTGTGTCACCTGCCAGACC CGCGGAAGAGC 900
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QY 1268 GTGCCCTTAGGGGTCTCTCTCAAGACGCACTGCCGCTGAGCTGCGGTACCCCGAGC 1327
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Db 1801 CAAGTTGCAAAACATTTGGAATCAGACAGACTTGAAGAGGTTGCAGCTGCCGGAGCTGTC 1860
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DEFINITION Human telomerase catalytic subunit promoter.
VERSION E36793.1 GI:13022756
KEYWORDS JP 1999253177-A/1.
SOURCE unidentifed.
ORGANISM unidentifed.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 1 21-SEP-1999;
JERON CORP,UNIVERSITY TECHNOLOGY CORP
OS Unidentifed
PN JP 1999253177-A/1
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724.643,18-APR-1997 US 08/844.419, PR
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MORIN,
PI CALVIN B HAREI,WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K48/00,
PC C12Q1/02,
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FT CDS 56..3454.

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Matches: 3979; Conservative		0;	Mismatches: 0; Indels: 36; Gaps: 1;
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QY	368	GCTGCTGGACGGGGCCCCGGGGGGCCCCCGAGGCGCTTTCACCAACAGCGTGGCGAGCTA	427
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QY	428	CCTGCCAACACACGGTGAACGACGACTGCGGGGAGCGGGCGTGGGGGCTGTGCTGGC	487
Db	421	CCTGCCAACACACGGTGAACGACGACTGCGGGGAGCGGGCGTGGGGGCTGTGCTGGC	480
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Db	481	CCGCGTGGGCGACGACGTGTGCTGTTCACTGTGACACGCTGCGCGCTTTGTGCTGTT	540
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Db	601	TCAGGCCCGCCCCCGCCACACAGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAAGGGC	660
QY	668	CTGGAACCAATAGCGTGAAGGAGGCGGGGTCCCTGAGCCCTGCCAGCCCGGGTGGAG	727
Db	661	CTGGAACCAATAGCGTGAAGGAGGCGGGGTCCCTGAGCCCTGCCAGCCCGGGTGGAG	720
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Db	721	GAGGCGCGGGGCGAGTGCAGCCGAAGTCTGCGCTTGGCCCAAGAGGCCAGGCGTGGCGC	780
QY	788	TGCCCCCTGAGCCGGAGGAGCGCCGCTTGGGCAAGGGTCTTGGGCCACCCGGGAGAGC	847
Db	781	TGCCCCCTGAGCCGGAGGAGCGCCGCTTGGGCAAGGGTCTTGGGCCACCCGGGAGAGC	840
QY	848	GCGTGGACCGAGTACCGTGGTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	907
Db	841	GCGTGGACCGAGTACCGTGGTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
QY	908	CACCTCTTTGGAGGCTGCGCTCTCTGGCACGCGCACTCCACCCATCCGCTGGCGGCCA	967

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Db	961	GCACACCGGGGGCCCCCATCCACATCGCGGCCACCAAGCTCCCTGGGACACGCTTGTCC	1020
QY	1028	CCCGGTGTACGGCCGAGACCAAGCACTTCTCTACTCTCCTCAGGGGACCAAGGACAGCTGGC	1087
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QY	1088	GCCCTCTTCTCTACTCTCAGCTCTCTGAGGCCCAAGCTGACCTGGGCTGGAGGCTGTGGA	1147
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QY	1448	GCGCTCTGTCGGGGCTGCTGCGCCGCGGCTGTGGCCCCCAGGCTCTGGGGCTCCAGGCA	1507
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RESULT 13

AF015950

LOCUS

DEFINITION

Homo sapiens telomerase reverse transcriptase (hTERT) mRNA, complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4015)
AUTHORS Nakamura,T.M., Morin,G.B., Chapman,K.B., Weinrich,S.L.,
Andrews,W.H., Lingner,J., Harley,C.B. and Cech,T.R.
TITLE Telomerase catalytic subunit homologs from fission yeast and human
JOURNAL Science 277 (5328), 955-959 (1997)
MEDLINE 97400623
PUBMED 9252327
REFERENCE 2 (bases 1 to 4015)
AUTHORS Morin,G.B.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-1997) Geron Corporation, 230 Constitution Drive,
Menlo Park, CA 94025, USA
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BASE COUNT 663 a 1363 c 1275 g 714 t
ORIGIN

Query Match 99.1%; Score 3969; DB 9; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-93;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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AUTHORS Meyerson,M., Counter,C.M., Eaton,E.N., Ellisen,L.W., Steiner,P., Caddle,S.D., Ziaugra,L., Beijersbergen,R.L., Davidoff,M.J., Liu,Q., Bacchetti,S., Haber,D.A. and Weinberg,R.A.
TITLE hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization
JOURNAL Cell 90 (4), 785-795 (1997)
MEDLINE 97433088
PUBMED 9288757
REFERENCE 2 (bases 1 to 4027)
AUTHORS Meyerson,M., Counter,C.M., Eaton,E.N., Ellisen,L.W., Steiner,P., Caddle,S.D., Ziaugra,L., Beijersbergen,R.L., Davidoff,M.J., Liu,Q., Bacchetti,S., Haber,D.A. and Weinberg,R.A.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1997) Whitehead Institute for Biomedical Research, Massachusetts Institute of Technology, Nine Cambridge Center, Cambridge, MA 02142, USA
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QY	1634	-----	1633
Db	35360	TGAGGTGCCAGGCCCTTGGTGAAGTGTGCGGTGTCCGGATGTGCAGGTCCGGG	35419
QY	1634	-----	1642
Db	35420	TGAGGTACACAGGCCCTCGGTGATCTGATGTGCATGTCCCTTCTCGTTAAGGGTTGG	35479
QY	1643	CTGTGTTCCGGCCGACAGACACCGCTGCGGTGAGAGATCCTGGCCAAGTTCCTGACTG	1702
Db	35480	CTGTGTTCCGGCCGACAGACACCGCTGCGGTGAGAGATCCTGGCCAAGTTCCTGACTG	35539
QY	1703	GCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTATGTACAGGAGACCAC	1762
Db	35540	GCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTATGTACAGGAGACCAC	35599
QY	1763	GTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGAGCAAGTTGCAAAACAT	1822
Db	35600	GTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGAGCAAGTTGCAAAACAT	35659
QY	1823	TGGAAT-----	1828
Db	35660	TGGAATCAGGTACTGTATCCCAAGCCAGGCTCTGCTTCGAACTCCTGAACACAG	35719
QY	1829	-----	1828
Db	35720	CCCGGCTCAGCATGCGCCTGTCTCCACTTGCTGTGCTTCCCTGCGTGCAGCTCTGG	35779
QY	1829	-----	1828
Db	35780	GCTGGAGCCAGGGCCCCGTCACAGGCTGTCTCAAGTGATTTCTGTCAAGGCTCTGA	35839
QY	1829	-----	1828
Db	35840	CTGCCTGAGCTCACGTTCTTCTTACTGTAAATCAGAGTTTGTGCCAAGTGTCTCTA	35899
QY	1829	-----	1828
Db	35900	GGGTTTGTAAAGCAGAAGGATTAAATTAGATGGAACACTACCACCTAGCCTCCCTGCC	35959
QY	1829	-----	1828
Db	35960	TTTCCCTGGGATGTGGGTCTGATTTCTCTCTTTTCTTTTGTGAGATGAGT	36019
QY	1829	-----	1828
Db	36020	CTCACTCTGTGCCCGAGGCTGAGTGCAGTGGCATATCTTGGCTCAGTCGAACCTCCAC	36079
QY	1829	-----	1828
Db	36080	CTCCTGGGTTTAAAGCATTCACCAGCCTCAGCCTCCTAAGTAGCTGGATTACAGCAC	36139
QY	1829	-----	1828
Db	36140	TGCCACCACGCCCTGCTAATTTTGTACTTTTAGAGAGACGGGTTTACCACTGTGGC	36199
QY	1829	-----	1828
Db	36200	CAGGCTGGTCTGGAATCATGACCTCAGGTGATCCACCACCTTGGCTGCCAAAGTGT	36259
QY	1829	-----	1828
Db	36260	GGGTTTACAGGCTAAGCCACCGTGGCCAGCCCCGATTCTCTTTAATTCATGCTGTCT	36319
QY	1829	-----	1828
Db	36320	GTAATGAATCTCAATCTATTGGATTAGGTATGAGAGATAAATCCACCACTTGGC	36379
QY	1829	-----	1828
Db	36380	GACTCACTGCAGGGAGCACCTGTGCAGGAGCACCTGGGGATAGAGAGATTCCACCATGA	36439

[illegible]

[illegible]

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QY	2046	TTTCAGCGTGTCTACTACTACGAGCGGGCGCGCGCCCCCGGCTCTCTGGCGCTCTGTGCTG		2105
Db	38660	TTTCAGCGTGTCTCACTACGAGCGGGCGCGCGCCCCCGGCTCTCTGGCGCTCTGTGCTG		38719
QY	2106	GGCGTGGACGATATCCACAGCGGCTTGGCGCACTTCTGTCTGCGTGTGCGGGGCCAGGAC		2165
Db	38720	GGCGTGGACGATATCCACAGGGCTTGGCGCACTTCTGTCTGCGTGTGCGGGGCCAGGAC		38779
QY	2166	CCGCCGCGCTGAGCTGTA-----	-----	2182
Db	38780	CCGCCGCGCTGAGCTGTACTTTGTCAAGTGTGGTGC CGGGGACCCCGGTGAGCAGCGCTGC		38839
QY	2183	-----	-----	2182
Db	38840	TGACCTTGGAGTGGCTGCTGATTGGCACCTCATGTTGGGTGAGAGGTA CTCTCTGG	-----	38899
QY	2183	-----	-----	2182
Db	38900	GTGGCGCCGACAGGAGTGCAGGTGACCCTGTCACTGTGAGGACACACCTGGCACCTAAGG	-----	38959
QY	2183	-----	-----	2182
Db	38960	TGAGGCGCTTCAGCGCTTTCCTGACGACACATGCGGGCCGACCTGTGACCTGACCCGGG	-----	39019
QY	2183	-----	-----	2182
Db	39020	CTCCTATTCCCAAGGAGGGTCCCACTGATTTCCAGTTTCCGTCAGAGAAGAACCGCAAC	-----	39079
QY	2183	-----	-----	2182
Db	39080	GGCTCAGCCACCAGGCCCCGCGTGTGCTTGACACCCAGTCTGTAAGCAGGCGTCTCTGTCC	-----	39139
QY	2183	-----	-----	2182
Db	39140	TGAGGCTCAGAGAGGGGACACAGCCCGCTGCCCCCTGGGGTCTGAGTGTGGGGTCA	-----	39199
QY	2183	-----	-----	2182
Db	39200	GAGAGAGAGTGGGGGACACCGCCAGGCCCTGAGGGCAGAGTGATGTCTGAGTTT	-----	39259
QY	2183	-----	-----	2182
Db	39260	CTGCGTGCCACTGTAGTCTCTCGCCTCCACTCACACAGGTGATGTGACGGCGCT	-----	39319
QY	2183	-----CATCCCCAGACAGGCTCACGGAGGTCAATCGCCAGCATATCAAAACCCAGA		2235
Db	39320	ACGACACCATTCCTCCCAAGACAGGCTCACGGAGGTATCGCCACGATATCAAAACCCAGA		39379
QY	2236	ACACGTAAGTGGCGTGGTATGCCCCGTGTCAGAGAAGCGGCCCATGGGACAGTCCGCA		2295
Db	39380	ACACGTAAGTGGCGTGGTATGCCCCGTGTCAGAGAAGCGGCCCATGGGACAGTCCGCA		39439
QY	2296	AGGCGTTCAAGAGCCAC-----	-----	2312
Db	39440	AGGCGTTCAAGAGCCACGTAAGGTTCAAGGTGATAGTGTGTCCAGATGTGTGTCT		39499
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Db	39500	GGGATATGAATGTGTCTAGATGCAGTCTGTCTGTGATGCGTTCTGTGCTGAGGTAC	-----	39555
QY	2313	-----	-----	2312
Db	39560	TTCCATGATTACACATCTGTGATATGCGTGTGGCACGTTGTGTGCTGTGATGTA	-----	39615
QY	2313	-----	-----	2312
Db	39620	TCTGTGGCGTGCATATTTGTGTGTGTGTGTGTGGCACAGTGTGTGTCCATGTGTGTG	-----	39675
QY	2313	-----	-----	2312

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QY	2679	-----AGACCCTGCTCCG	2692
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Db	53060	AGGTGTCCCTGAGTATGGCTGCGTGTGAACCTTCCGGAAGACAGTGTGTAACCTTCCCTGT	53119
QY	2753	AGAAAGCAGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCC	2812
Db	53120	AGAAAGCAGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCC	53179
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Job time : 11057 secs


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: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 224:
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:   STRANDEDNESS: single
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:     NAME/KEY: CDS
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: SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224

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Matches 3979; Conservative	0;	Mismatches	0;	Indels 36; Gaps 1;

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RESULT 2
US-09-953-052-1
Sequence 1, Application US/09953052
Patent No. US20020173476A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "human telomerase reverse
transcriptase (hTRT)"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1
Query Match 99.1%; Score 3969; DB 9; Length 4015;
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Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
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RESULT 3
US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

TITLE OF INVENTION: NO. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
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US-10-053-758-224
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QY	488	CCGGGTGGCGACGACGTGCTGTTCACTGCTGGCACGCTGGCGGCTCTTTGTGCTGT	547
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QY	1328	AGCGGCTGTCTGTGCCCCGGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCCCGAGAGGAGGA	1387

Dp	1321	AGCGGCTGTCTGTGGCCCGGGAGAAAGCCCGCAGGGCTCTGTGTGGCGGCCCGCCGAGAGAGAGA	1380
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QY	1868	GGAAGCAGAGGTTCAGGCGACGATCGGGGAAGCCAGGCCCGCCCTGCTGACGCTCCAGACTCCG	1927
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RESULT 4
US-10-054-295-224
Sequence 224, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054, 295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854, 050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846, 017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/844, 419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/724, 643
FILING DATE: 01-Oct-1996

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;
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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;
US-10-054-295-224

Query Match          99.1%; Score 3969; DB 9; Length 4015;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY      8 GCAGGCGCTGCGTCTGCTGCGCAGCTGGAGAGCCCTGGCCCCGGCCACCCCGCGATGCC 67
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QY      248 ACGGCGCGCGCGCGCGCGCGCGCTTCCCGCAGGTGTCTGCTGCTGAAGAGCTGTGGC 307
Db      241 ACGGCGCGCGCGCGCGCGCGCGCTTCCCGCAGGTGTCTGCTGCTGAAGAGCTGTGGC 300

QY      308 CCGAGTGTGACAGAGGCTGTGCGAGCGCGGCGGAGAGACGTGCTGGCTTCGGCTTCGC 367
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QY      1208 GCGCCAGCGCTACTGGAATGCGGCCCTGTTCTGAGCTGCTTGGGAACACGCGCA 1267
Db      1201 GCGCCAGCGCTACTGGAATGCGGCCCTGTTCTGAGCTGCTTGGGAACACGCGCA 1260
QY      1268 GTGCCCCCTACGGGGGTGCTCTCAAGAGCAGCTGCGCGCTGCGAGCTGCGGTCAACCCAGC 1327
Db      1261 GTGCCCCCTACGGGGGTGCTCTCAAGAGCAGCTGCGCGCTGCGAGCTGCGGTCAACCCAGC 1320
QY      1328 AGCGGCTGTCTGCGCGGAGAGAGCCCGAGGGCTGTGCGGGCGCCCGAGAGAGAGA 1387
Db      1321 AGCGGCTGTCTGCGCGGAGAGAGCCCGAGGGCTGTGCGGGCGCCCGAGAGAGAGA 1380
QY      1388 CACAGACCCCGCTGCGCTGTGAGCTGCTCCGCGCAGCAGACAGACGCCCTGGCAGGTGA 1447
Db      1381 CACAGACCCCGCTGCGCTGTGAGCTGCTCCGCGCAGCAGACAGACGCCCTGGCAGGTGA 1440
QY      1448 CCGCTTGTGCGGGGCGCTGCGCTGCGCGGCGCTGTGCGGCCAGGCTCTGGGGCTCAAGGA 1507
Db      1441 CCGCTTGTGCGGGGCGCTGCGCTGCGCGGCGCTGTGCGGCCAGGCTCTGGGGCTCAAGGA 1500
QY      1508 CAAGAACGCGCGCTTCTCAGGAACACCAAGATCATCTCCCTGGGGAAGCATGCCAA 1567
Db      1501 CAAGAACGCGCGCTTCTCAGGAACACCAAGATCATCTCCCTGGGGAAGCATGCCAA 1560
QY      1568 GCTCTGCTGACGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGCAG 1627
Db      1561 GCTCTGCTGACGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGCAG 1620
QY      1628 GAGCCAGGGGTTGGCTGTCTCCGCGCAGAGACCGCTGCGTGAGAGAGATCTGGC 1687
Db      1621 GAGCCAGGGGTTGGCTGTCTCCGCGCAGAGACCGCTGCGTGAGAGAGATCTGGC 1680
QY      1688 CAAGTCTCTGCACTGGCTGATGAGTGTGTACGTGCTGAGAGCTGCTCAGGCTCTTCTTTA 1747
Db      1681 CAAGTCTCTGCACTGGCTGATGAGTGTGTACGTGCTGAGAGCTGCTCAGGCTCTTCTTTA 1740
QY      1748 TGTACGAGAGACAGTTCATAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG 1807
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Db 1741 TGTACGGAGACCACGTTTCAAAAGACAGGCTCTTTTCTACCGAAGAGTGTCTGGAG 1800
QY 1808 CAAGTTGCAAGCATTTGGAATCAGACAGCATTGAAGAGGGTGCAGCTGCGGAGCTGTC 1867
Db 1801 CAAGTTGCAAGCATTTGGAATCAGACAGCATTGAAGAGGGTGCAGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTTCAGGACGATCGGGAAGCCAGGCCCGCTGTGAGCTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTTCAGGACGATCGGGAAGCCAGGCCCGCTGTGAGCTCCAGACTCCG 1920
QY 1928 CTTTCATCCCCAAGCCTGACGGGCTCGGCCGATTTGTGAACATGGAATACTGTCGGAGC 1987
Db 1921 CTTTCATCCCCAAGCCTGACGGGCTCGGCCGATTTGTGAACATGGAATACTGTCGGAGC 1980
QY 1988 CAGAAGCTTCCGACAGAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCATGTT 2047
Db 1981 CAGAAGCTTCCGACAGAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCATGTT 2040
QY 2048 CAGCGTGTCACTACGAGCGGGCGGGCCCGCCCGCTCCTGGCGCTCTGTGCTGGG 2107
Db 2041 CAGCGTGTCACTACGAGCGGGCGGGCCCGCCCGCTCCTGGCGCTCTGTGCTGGG 2100
QY 2108 CCTGACGATATCCACAGGGCCTGGCGCACTTCGTGCTGCTGCTGCGGGCCAGAGACC 2167
Db 2101 CCTGACGATATCCACAGGGCCTGGCGCACTTCGTGCTGCTGCTGCGGGCCAGAGACC 2160
QY 2168 GCCGCTGAGCTGTA-----CATCCCCCA 2191
Db 2161 GCCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGGCTACGACACCATCCCCCA 2220
QY 2192 GGACAGGCTCACGGAGTTCATCGCCAGCATCATCAACCCCGAAGACAGTACTGCTGGC 2251
Db 2221 GGACAGGCTCACGGAGTTCATCGCCAGCATCATCAACCCCGAAGACAGTACTGCTGGC 2280
QY 2252 TCGGTATGCCGTGTGTCAGAAAGGCCCGCCATGGGCACGTCCGCAAGGCTTCAAGAGCCA 2311
Db 2281 TCGGTATGCCGTGTGTCAGAAAGGCCCGCCATGGGCACGTCCGCAAGGCTTCAAGAGCCA 2340
QY 2312 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCCTGACGA 2371
Db 2341 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCCTGACGA 2400
QY 2372 GACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2431
Db 2401 GACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2460
QY 2432 CAGTGGCCTTTCGACGTTTCTAAGCTTCATGTGCGCACACCGCGTGCATCAGGGG 2491
Db 2461 CAGTGGCCTTTCGACGTTTCTAAGCTTCATGTGCGCACACCGCGTGCATCAGGGG 2520
QY 2492 CAAGTCTTACGTTCCAGTGCAGGGGATCCCGCAGGGGCTCCATCCTTCCACGCTGCTGTG 2551
Db 2521 CAAGTCTTACGTTCCAGTGCAGGGGATCCCGCAGGGGCTCCATCCTTCCACGCTGCTGTG 2580
QY 2552 CAGCCTGTGCTACGGCGACATGGAACAAGCTGTTGCGGGGATTCGGCGGAGCGGGCT 2611
Db 2581 CAGCCTGTGCTACGGCGACATGGAACAAGCTGTTGCGGGGATTCGGCGGAGCGGGCT 2640
QY 2612 GCTCCTGCGTTTGGTGATGATTTCTTGTGGTGACACCTCACCCTCACCCACGGAAGAAC 2671
Db 2641 GCTCCTGCGTTTGGTGATGATTTCTTGTGGTGACACCTCACCCTCACCCACGGAAGAAC 2700
QY 2672 CTTCTCAGGACCCCTGTCGAGGTGTCCTTGAGTATGGCTGCGTGTGAACCTTGGCGAA 2731
Db 2701 CTTCTCAGGACCCCTGTCGAGGTGTCCTTGAGTATGGCTGCGTGTGAACCTTGGCGAA 2760
QY 2732 GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTGTTCAGAT 2791
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QY 2792 GCCGCGCCACGGCCTATTCCTCGTGGCGGCTGCTGCTGATACCCGAGACCTGAGGT 2851
Db 2821 GCCGCGCCACGGCCTATTCCTCGTGGCGGCTGCTGCTGATACCCGAGACCTGAGGT 2880

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Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGAAACTCTTTGGGGTCTTGGGCTGAAGTG 3000
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Db 3001 TCACAGCCTTTTCTGGATTTGCAGTGAACAGCCCTCCAGACGCTGTGCACCAACATCTA 3060
QY 3032 CAAGATCTCTCTGCTGCAGGCGTACAGCTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3091
Db 3061 CAAGATCTCTCTGCTGCAGGCGTACAGCTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
QY 3092 TCAGCAAGTTTGAAGAACCACATTTTCTGCGCGTCACTCTGACAGCGCTCCCT 3151
Db 3121 TCAGCAAGTTTGAAGAACCACATTTTCTGCGCGTCACTCTGACAGCGCTCCCT 3180
QY 3152 CTGCTACTCATCTTGAAGCCAAAGACGAGGGATGTCGCTGGGGCCAAAGGCGCGCG 3211
Db 3181 CTGCTACTCATCTTGAAGCCAAAGACGAGGGATGTCGCTGGGGCCAAAGGCGCGCG 3240
QY 3212 CGGCCCTGTGCCCCCTCCGAGGCGCTGCAGTGGCTGTGCCACCAAGCATTCCTGCTAAGCT 3271
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QY 3272 GACTCGACACCTGTACACCTACGTGCCACTCTGGGTCACTCAGSACAGCCAGAGCGCA 3331
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QY 3332 GCTGAGTCGAAGCTCCCGGGGAGCAGCCTGACTGCCCTGGAGGCGCGCAACCCGCGC 3391
Db 3361 GCTGAGTCGAAGCTCCCGGGGAGCAGCCTGACTGCCCTGGAGGCGCGCAACCCGCGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACCCGCGCAAGCCAGGCGCA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACCCGCGCAAGCCAGGCGCA 3480
QY 3452 GAGCAGACACGACGACCCCTGTACGGCGGGCTCTACGTCCACGAGGAGGAGGGCGGCC 3511
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QY 3632 GAGTGTCCAGACACACTGCCGCTTTCACCTTCCACAGGCTGGCGCTCGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACACTGCCGCTTTCACCTTCCACAGGCTGGCGCTCGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCTCACCAGAGGCCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTTCTCACCAGAGGCCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTCGCATTTGTTCACCCCTCGCCCTGCCCCCTTGTGCTTCCACCCACCATCC 3811
Db 3781 CCAGATTCGCATTTGTTCACCCCTCGCCCTGCCCCCTTGTGCTTCCACCCACCATCC 3840
QY 3812 AGGTGAGACCTTGAGAAGACCTTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3871
Db 3841 AGGTGAGACCTTGAGAAGACCTTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGCGGAGGACCTGCACCTGATGGGGTCCCTGTGGGTCAATTTGGGG 3931
Db 3901 CCCTGTACACAGCGGAGGACCTGCACCTGATGGGGTCCCTGTGGGTCAATTTGGGG 3960

DB	3781	CCAGATTGCCATTGTTCCACCCCTCGCCCTGCTCCTTGGCTTCCACCCCCACCATCC	3840
QY	3812	AGGTGGAGACCCCTGGAGAGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG	3871
Db	3841	AGGTGGAGACCCCTGGAGAGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG	3900
QY	3872	CCCTGTACACAGGCGGAGGACCCCTGCACCTGATATGGGGGTCCCTGTGGTCAATTTGGGGG	3931
Db	3901	CCCTGTACACAGGCGGAGGACCCCTGCACCTGATATGGGGGTCCCTGTGGTCAATTTGGGGG	3960
QY	3932	GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGGAAAAAA	3986
Db	3961	GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGGAAAAAA	4015

QY	968	GCACCA	CGCGGGCCCCCATTCACATCGCGGCGCCACACGTCCTCGGACACACGCGCTTGCC	1027
Db	961	GCACCA	CGCGGGCCCCCATTCACATCGCGGCGCCACACGTCCTCGGACACACGCGCTTGCC	1020
QY	1028	CCCCGT	GTACGCCGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAAGAGACAGCTGCG	1087
Db	1021	CCCCGT	GTACGCCGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAAGAGACAGCTGCG	1080
QY	1088	GCCCCT	CTCTACTAGCTCTGTAGGCCCCAGCCCTGACTGGCGCTCGGAGGCTCGTGA	1147
Db	1081	GCCCCT	CTCTACTAGCTCTGTAGGCCCCAGCCCTGACTGGCGCTCGGAGGCTCGTGA	1140
QY	1148	GACCAT	TCTTCTGGGTTCCAGGGCCCTGGATGCCAGGGACTCCCCGAGGTGCCCCGCT	1207
Db	1141	GACCAT	TCTTCTGGGTTCCAGGGCCCTGGATGCCAGGGACTCCCCGAGGTGCCCCGCT	1200
QY	1208	GCCCCA	GCGCTACTTGCCAAATGCGCCCCCTGTGTTCTGAGCTGCTTGGAAACCAAGCGCA	1267
Db	1201	GCCCCA	GCGCTACTTGCCAAATGCGCCCCCTGTGTTCTGAGCTGCTTGGAAACCAAGCGCA	1260
QY	1268	GTGCCC	CTACGGGGGTGTCCTCAAGACGCACGTGCCCGCTGCGAGCTGCGGTCAACCCAGC	1327
Db	1261	GTGCCC	CTACGGGGGTGTCCTCAAGACGCACGTGCCCGCTGCGAGCTGCGGTCAACCCAGC	1320
QY	1328	AGCCGG	TGTGTGCCCCGGAGAGAAGCCCCAGGGCTCTGTGGCGGGCCCCCGAGAGAGAGA	1387
Db	1321	AGCCGG	TGTGTGCCCCGGAGAGAAGCCCCAGGGCTCTGTGGCGGGCCCCCGAGAGAGAGA	1380
QY	1388	CACAGAC	CCCCCGTCGCCCTGGTGCAAGCTGCTCCGCCACAGACAGACGCCCTGGCAGGTGTA	1447
Db	1381	CACAGAC	CCCCCGTCGCCCTGGTGCAAGCTGCTCCGCCACAGACAGACGCCCTGGCAGGTGTA	1440
QY	1448	CGGCTT	CGTGCGGGGCGCTGCGCTGCGCGCGCTGTGTGCCCAAGGCGCTCTGGGGCTCCAGCA	1507
Db	1441	CGGCTT	CGTGCGGGGCGCTGCGCTGCGCGCGCTGTGTGCCCAAGGCGCTCTGGGGCTCCAGCA	1500
QY	1508	CAACGA	ACGCGCGCTTCTCAGGAACACCAAGAACTTCCTCTGGGAAGCATGCCAA	1567
Db	1501	CAACGA	ACGCGCGCTTCTCAGGAACACCAAGAACTTCCTCTGGGAAGCATGCCAA	1560
QY	1568	GCTCTC	GTGTCAGAGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTC	GTGTCAGAGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCC	AGGGGTGGCTGTGTTCCGGCCGACAGAGCACCCGCTGCGTGAGGAGATCCTGGC	1687
Db	1621	GAGCCC	AGGGGTGGCTGTGTTCCGGCCGACAGAGCACCCGCTGCGTGAGGAGATCCTGGC	1680
QY	1688	CAAGTT	CTGTGACCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTTTCTTTTA	1747
Db	1681	CAAGTT	CTGTGACCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTTTCTTTTA	1740
QY	1748	TGTCAC	GAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCAC	GAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTT	GCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC	1867
Db	1801	CAAGTT	GCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC	1860
QY	1868	GGAAGC	AGAGTCAAGCATCGGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGC	AGAGTCAAGCATCGGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCAT	CCCCAAGCCTGACGGGCTGCGGCGGATTTGTGAACATGGAATACTAGTCTGGAGC	1987
Db	1921	CTTCAT	CCCCAAGCCTGACGGGCTGCGGCGGATTTGTGAACATGGAATACTAGTCTGGAGC	1980
QY	1988	CAGAAG	CTTCCGACAGAAAAGAGGGCCGAGCGTCTACCTCGAAGGTTGAAGGCACCTGTT	2047
Db	1981	CAGAAG	CTTCCGACAGAAAAGAGGGCCGAGCGTCTACCTCGAAGGTTGAAGGCACCTGTT	2040

QY	2048	CAGCGTGCCTCAACTACGACGCGGGCGGGCGCCCCCGGCTTCCTGGGGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGCCTCAACTACGACGCGGGCGGGCGCCCCCGGCTTCCTGGGGCGCTCTGTGCTGGG	2100
QY	2108	CCTGGACGATATCCACAGGCGCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAGAGACC	2167
Db	2101	CCTGGACGATATCCACAGGCGCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAGAGACC	2160
QY	2168	GCCGCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCGCTGAGCTGTACTTTGTCAAAGGTGATGTGACGGGGCGGTACGACACCATCCCCCA	2220
QY	2192	GGACAGGCTCACGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACGTA CTGCGTGG	2251
Db	2221	GGACAGGCTCACGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACGTA CTGCGTGG	2280
QY	2252	TGCGTATGCCGTGGTCCAGAGGCCGCCCATGGGCACGTCCGCAAGGCCCTCAAGAGCCA	2311
Db	2281	TGCGTATGCCGTGGTCCAGAGGCCGCCCATGGGCACGTCCGCAAGGCCCTCAAGAGCCA	2340
QY	2312	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGCAGGA	2371
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGCAGGA	2400
QY	2372	GACCAAGCCCGCTGAGGGATGCGGTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCGAG	2431
Db	2401	GACCAAGCCCGCTGAGGGATGCGGTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCGAG	2460
QY	2432	CAGTGGCCTCTTCGACGTCCTCCACGCTTACGCTTCATGTGCCACCAAGCCGCTGCGATCAGGG	2491
Db	2461	CAGTGGCCTCTTCGACGTCCTCCACGCTTACGCTTCATGTGCCACCAAGCCGCTGCGATCAGGG	2520
QY	2492	CAAGTCCCTACGTCCAGTGCAGGGGATCCCGCAGAGGGCTCCATCCTCTCCACGCTGCTCTG	2551
Db	2521	CAAGTCCCTACGTCCAGTGCAGGGGATCCCGCAGAGGGCTCCATCCTCTCCACGCTGCTCTG	2580
QY	2552	CAGCCTGTGCTACGGCGCAGATGAGAGAACAAGCTGTTGCGGGGATTCGGCGGAGCGGCT	2611
Db	2581	CAGCCTGTGCTACGGCGCAGATGAGAGAACAAGCTGTTGCGGGGATTCGGCGGAGCGGCT	2640
QY	2612	GCTCTGCGCTTGGTGATGATTTCTTGTGTGTGACACCTCACTCACCCACGCGGAAC	2671
Db	2641	GCTCTGCGCTTGGTGATGATTTCTTGTGTGTGACACCTCACTCACCCACGCGGAAC	2700
QY	2672	CTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGCTGTAACCTTGGCGAA	2731
Db	2701	CTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGCTGTAACCTTGGCGAA	2760
QY	2732	GACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT	2791
Db	2761	GACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT	2820
QY	2792	GCCGCGCCACAGGCGCTATTCCTGCTGGTGGGCTGTGCTGATACCCGGACCCTGAGGT	2851
Db	2821	GCCGCGCCACAGGCGCTATTCCTGCTGGTGGGCTGTGCTGATACCCGGACCCTGAGGT	2880
QY	2852	GCAGAGCGACTACTCCAGCTATGCCCGGACCCTCCATCAGAGCCAGTCTCACCTTCAACCG	2911
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QY	2912	CGGCTTCAAGGCTGGGAGAGACATGCGTGGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	2971
Db	2941	CGGCTTCAAGGCTGGGAGAGACATGCGTGGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
QY	2972	TCACAGCCTGTTTCTGATTTGACAGGTGAACAGCCTCCAGACGGGTGTGCACCAACATCTA	3031
Db	3001	TCACAGCCTGTTTCTGATTTGACAGGTGAACAGCCTCCAGACGGGTGTGCACCAACATCTA	3060
QY	3032	CAAGATCCTCTCTGCTGCAGGCGTACAGGTTTACACGCATGTGTGCTGCAGCTCCCATTTCA	3091
Db	3061	CAAGATCCTCTCTGCTGCAGGCGTACAGGTTTACACGCATGTGTGCTGCAGCTCCCATTTCA	3120
QY	3092	TCAGCAAGTTTGAAGAACCACATTTTCTGCTGGCGCTCATCTCTGCACAGGCGCTCCT	3151

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Db 3181 CTGCTACTCCATCCTGAAAGCCAAAGACGAGGATGTCGCTGGGGGCCAAGGGCGCCG 3240
QY 3212 CGGCCCTCTGCCCCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271
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QY 3332 GCTGAGTGGGAAAGCTCCCGGGGAGAGAGCTGACTGCCCTGGAGCGCGACACCCGCGC 3391
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QY 3752 CCAGATTCGCTATGTCACCCCTGCGCTGCCCTTGTGCTTGCCTCCACCCCACTCC 3811
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Db 3901 CCCTGTACACAGGCGAGGACCTTGACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGG 3960
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RESULT 7
US-10-105-963-1
; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; TITLE OF INVENTION: Recombination
; FILE REFERENCE: 731/002

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; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-105-963-1

Query Match          99.1%; Score 3969; DB 9; Length 4015;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCGTCTGCTGCGACGTGGAGCCCTGGCCCCGGCCACCCCCGGAGTGGC 67
Db 1 GCAGCGCTGCGTCTGCTGCGACGTGGAGCCCTGGCCCCGGCCACCCCCGGAGTGGC 60
QY 68 GCGCGCTCCCGCTGCGGAGCGGTGCGTCTGCTGCGAGCCACTACCGCGAGGTGCT 127
Db 61 GCGCGCTCCCGCTGCGGAGCGGTGCGTCTGCTGCGAGCCACTACCGCGAGGTGCT 120
QY 128 GCGCGTGGCCACGTTCGTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGTGACGCGG 187
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QY 188 GGACCCGGCGGCTTTCGCGCGCTGGTGCGCCAGTGCCTGCTGCTGCGCTGGGACGC 247
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QY 248 ACGGCGCGCGCGCGCGCGCGCTTCCCGAGAGTGTCTGCTGCTGAAGAGTGTGGC 307
Db 241 ACGGCGCGCGCGCGCGCGCGCTTCCCGAGAGTGTCTGCTGCTGAAGAGTGTGGC 300
QY 308 CCAGTGTCTGACAGGCTGTGAGAGCGCGCGCGGAAGACGTGCTGCGCTTGGCTTCCG 367
Db 301 CCAGTGTCTGACAGGCTGTGAGAGCGCGCGCGGAAGACGTGCTGCGCTTGGCTTCCG 360
QY 368 GCTGCTGAGAGCGCGCGCGCGCGCGCGCGAGGCTTCAACACAGCGTGGCGACTA 427
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QY 428 CCGCGCAACAGGCTGACGAGCGCACTGCGGGGAGAGCGGGCGTGGGGCTGCTGTCG 487
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QY 488 CCGCGTGGCGAGACGTGCTGTTACCTGCTGGACGCTGCGCGCTTGTGTGCTGTG 547
Db 481 CCGCGTGGCGAGACGTGCTGTTACCTGCTGGACGCTGCGCGCTTGTGTGCTGTG 540
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Db 721 GAGCGCGGGGGGAGTGCAGCGCGAAGTTCGCTTGGCCCAAGAGGCCAGGCGTGGCGC 780
QY 788 TGCCCTGAGCCGAGCGGAGCGCGCGTGGGCAAGGGGTCTGGGCCCAACCCGGGCGAGGAC 847

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QY 3032 CAAGATCCTCTGCTGCAAGGCGTACAGGTTTCAAGCATGTGTGCTGCAGCTCCCATTTTCA 3091
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US-09-733-294A-3
; Sequence 3, Application US/09733294A

; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William M. Gaarde
; APPLICANT: Susan M. Freiler
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56) ... (3454)
US-09-733-294A-3

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RESULT 10
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; Sequence 30, Application US/09733294A
; Patent No. US2002045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Query Match	95.9%;	Score 3843.4;	DB 10;	Length 51552;
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Db	11272	CGATGCCGCGCGCTCCCCGCTGCCAGCCGTGCGTCCCTGCTGCGCAGCCACTACCGG	11331
OY	121	AGGTGCTGCCGCTGGCCACGTTGCTGCGCGCCTGGGGCCCCAGGGCTGGCGGTGTGC	180
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[illegible][illegible]

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QY 2679 ----- 2678

Db 37672 TGCTCACCTACCTGTCTCTGCCCCGGAGACAGGGAAGCACACCCCGAAGTCTGAGCAGGGC 37731
QY 2679 ----- 2678
Db 37732 TGGTCCAGGCTCCTCAGAGCTCCTTGCCAGGCCACACCCTGCTCCAATCACCACCTTC 37791
QY 2679 ----- 2678
Db 37792 TCTGGGTTTCCAAAGCATTTAACAAGGGTGTACAGTTACCTTCCTGGGTGACGGCCCCG 37851
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Db 37852 CATCTGGGGCTGACATTGCCCCCTGTGCTTAGGACCCCTGTCGAGGTTGCCCTGAGTA 37911
QY 2708 TGGCTGCGTGTGAACCTTGCGAAGACAGTGTGAACCTTCCCTGAGAAGCAGAGGCCCT 2767
Db 37912 TGGCTGCGTGTGAACCTTGCGAAGACAGTGTGAACCTTCCCTGAGAAGCAGAGGCCCT 37971
QY 2768 GGGTGGCAGGCTTTTGTTCAGATGCGCGCCACAGGCCCTATTCCTGCTGCGGCCCTGCT 2827
Db 37972 GGGTGGCAGGCTTTTGTTCAGATGCGCGCCACAGGCCCTATTCCTGCTGCGGCCCTGCT 38031
QY 2828 GCTGATACCCGGAACCTTGAGGTTGACAGCGACTACTC----- 2866
Db 38032 GCTGATACCCGGAACCTTGAGGTTGACAGCGACTACTCAGGTGAGCGCACCTGCGCCG 38091
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Db	38992	TGCAGTGAGCCGAGATCACACCAGCTGCAGCCTGGGCAACAGAGTGAGACTTCATC	39051
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Db	39172	TCTGAAGGCACACCTTCATGGGAAGAAATAAGTGGTGAATGTTGTTAAACCAGAGG	39231
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Db	39232	TTTAACTGGGGTCCGTGCTTCGAGTTAACAGTCCAGATCTGGACTTTGCCCTTTCC	39291
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Db	39352	GGGAGCAGAGGTGACAGACGCCCTCATGATGGGGAGTGGCAGGTGCAGACACCCTTGTG	39411
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Db	39412	CATGTGCCCAAGCATGTCCTGTTGCACTCCCTCCCAAGAGATGCCGGTCTCCTGTG	39471
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Db	39472	CTCCCAACAGTCCCTGCTTCCCTTCACAGCCTTAACCTGTCTGGCCTCCACTGGCTTT	39531
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Db	39532	GTCGTGATGATTTCCACATTTCCGTGGGCTCCAGACACTCTTCGCCCTCTCCAGGCACT	39591
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Db	39592	CTGAGTGTGGCCATACCAAGTCACTGTGAAGTCCACTGCTTATTTTGTCTCCCATG	39651
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Db	39652	AAATGATTTTTTAGGACAGGACCCCTGTTCCAGCCTCTGGCACAGCATAGTGAATG	39711
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Db	39712	TTATTGAAGGACAAAGACAGACAACAATCAGGAAAAATGGTTCTCTTAACACATTT	39771
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Db	39772	GCAATGCCACAGAGGCTAGTGACGATGGGTGGGCATCAGTCAATCAGATGGGTCCAA	39831
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Db	39832	TGCCAGATATTTCTGTGCTCCCAAGGCCACTTGTGTCAGAGTGTGCTTGACAGAGTGG	39891

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Db	40072	TCTCCCAAACCAAGCTCAGATGGTAGAATGTGTCAGAACTGATGCACAGAACATAGA	40131
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Db	40132	ACAAAACGGAAGCCCTATCTCTCAGAAAGTGTGTTAATGTGTATGTGGCACAGCTGAT	40191
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Db	40192	GGAAAAGAGTGTGTGTATTTTTTTTCTGAGAAACTGACTGGAAGCAATAAGT	40251
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Db	40372	TTGCTGTTGGGGAAGACACACAGGAGGGGATGAACCAAGTAGGCAACGGGCAATTGC	40431
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Db	40432	TTTCACTGACAGAAACTCAGCTTGCCTGAGCCACAGTGAATAATGGCCATTTCCCTGAGC	40491
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Db	40492	GTTGTGCACGTGATTTATTAAAGCGCCCTGTGAGTCTTGACATTCATCCTCTCACT	40551
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Db	40552	TTGTTCTCTAACCACTGAGAGGTAGAGAGGAAAGGCTCCAGGGAGCAGCCGCCCTT	40611
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Db	40612	GGTCACCCAGCTGGCAAAAGGCATGCATGATTCAGAGCCTGGCCTCTGCTCCGGGGCCCT	40671
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Db	40672	TGCTCTGCCGAGAGACCCACACAAGTCAGACCCATAGGCTCAGGGTGAGCCGAGCCCA	40731
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Db	40732	AGGTGCTGTTGGGGATGGCTGTGAAGAAATGACGCTCTGATGCACACTTGGAAGG	40791
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Db	40792	TCCTAACAGAGCCTCAAGAATAATGCATGTGAACCTGACAGCGAGACCCATCCCTCAAG	40851
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Db	40852	AAACGCACGTGAAACTGATGCGGAGACCTGTCCCCATCCTCATGCTGCTCTTTCTG	40911
QY	2867	-----	2866
Db	40912	GGCTTGCCAAGACCAGCATCAGGTTGAGGCAAGCTGGAAAAGACTTTTCTGAAAGCAGC	40971
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Db 47152 CTCTGGGGTCACTCAGACAGCAAGTGTGGTGAGGCCAGTGGGCCACCTGCC 47211
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QY 3319 ----- 3318
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Db 47632 CCACCCACACGTCCTAGAGGGTTGAGGATGCCACTCTGCGCTTCTTGAAACGGAGT 47691
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RESULT 11

US-09-843-676-173
Sequence 173, Application US/09843676
Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
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REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: 1..4029
LOCATION: /note= "preliminary sequence for
human TRF cDNA insert of
plasmid pGRN121"
SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-09-843-676-173

Query Match 95.7%; Score 3832.6; DB 9; Length 4029;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;

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QY 68 GCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGACGCACTACCGGAGTGCT 127
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QY 128 GCGCGCTGCGACGTTCGTGCGCGCCCTGGGGCCCCAGGGCTGCGGCTGTGACGCGCG 187
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Db	421	CCTGCGCAACACAGGTGACACCGACGCTGCGGGGGAGACGGGGGGCTGGGGGGCTGCTCTGGC	480
QY	488	CCGCGTGGGGCGACGACGTGCTGGTTACCTGCTGGACAGCTGGCGGCTCTTTGTCTGTGT	547
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QY	548	GGCTCCAGCTGCGCCTACCAAGGTGCGGGGCGCGCTGTACCAGTCCGGCGCTGGCCAC	607
Db	541	GGNTCCCACTGCGCCTTACCANGTGTGGCGGCGCGCGCTGTACCAGTCCGGCGCTGGCCAC	600
QY	608	TCAGGCGCGCGCGCGCGCACACGCTAGTGGACCCCGAAAGCGTCTGGGATGCGAAGCGGC	667
Db	601	TCAGGCGCGCGCGCGCGCACACGCTANTGGA - CCCGAAGCGTCTGGGAT - CCAACGGGC	658
QY	668	CTGGAACCATAGCGTCAAGGAGGAGCGGGGTCGCCCTGGGGCTGCCAGCCCCGGGTGGCAG	727
Db	659	CTGGAACCATAGCGTCAAGGAGGAGCGGGGTCGCCCTGGG - CTGCCAGCCCCGGGTGGCAG	717
QY	728	GAGGCGCGGGGGCAGTGCACGCGGAAGTCTGCCGTTGCCCAAGAGCGCCAGGCTGGCGC	787
Db	718	GAGGCGCGGGGGCAGTGCACGCGGAAGTCTGCCGTTGCCCAAGAGCGCCAGGCTGGCGC	777
QY	788	TGCCCCGTAGCCCGGAGCGGAGCGCCGCTGGGCAAGGGTCTGGGCCACCCGGCGAGAC	847
Db	778	TGCCCCGTAGCCCGGAGCGGAGCGCCGCTGGGCAAGGGTCTGGGCCACCCGGCGAGAC	837
QY	848	GCGTGAACGAGTGAACCGTGGTTCTGTGTGGTGTACCTGCAGACCCGCCGAAGAAGC	907
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QY	908	CACCTCTTTGGAGGGTGGCGCTCTCTGGCACCGCGCCACTGCCACCCACTCCGTGGCGGCCA	967
Db	898	CACCTCTTTGGAGGGTGGCGCTCTCTGGCACCGCGCCACTGCCACCCACTCCGTGGCGGCCA	957
QY	968	GCACACAGCGGGGCCCCCATCCATCGCGGCCACACAGCTCCCTGGGACACGCTTGTCC	1027
Db	958	GCACACAGCGGGGCCCCCATCCATCGCGGCCACACAGCT - CCTGGACACGCTTGTCTCC	1016
QY	1028	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTAGGCGACAAAGAGCACTGGC	1087
Db	1017	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTAGGCGACAAAGAGCACTGGC	1074
QY	1088	GCCCTCTTCTCTACTC - AGCTCTGTAGAGGCCACGCTGACTGGCGCTC - GGAGGCTCGTG	1145
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QY	1146	GAGACCATCTTCTGGGTTCCAGGCCCCGTGATGCCAGGAACTCCCGCAGTTGGCCCCGC	1205
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QY	1266	CAGTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGGCCGCTGCGAGCTGGCGGTACCCCCA	1325
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Db	1313	GCAGCGGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTGTGTGGCGCCCCCGAGAGGAG	1372
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Db	1373	GAACACAGACCCCGCTGCGCTGTGTGACGTCTCCGCGACACAGACAGCCCTGGCAGGT	1432
QY	1445	GTAAGGCTTCGTGCGGGGCTGCTTCGCGCGGCTGTGTGCCCCCAGGCGCTCTGGGGCTCCAG	1504

Db	1433	GTACGGCTTCGTGCGGGCCTGCGCTGCGCGCGCGGTGGTGCCCGCCAGGCCCTTGCGGGCTCCAG	14922
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Db	1493	GCACAACGAAGCGCCGCTTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGGAAGCATGC	15522
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QY	1745	TTATGTCAGGGAGAGACCACTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTG	18044
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QY	1865	GTCCGAAGCAGAGGTTCAGGCGAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT	19244
Db	1853	GTCCGAAGCAGAGGTTCAGGCGAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT	19122
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Db	1913	CCGCTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACCTACGTCGTGG	19722
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Db	1973	AGCCAGAAGCTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAAGGTGAAGGCACCT	20322
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QY	2249	GCGTCGATATGCGGTGTCAGAAAGGCCGCCCATGGGCGACGTCCGCAAGGCCCTTCAAGAG	23082
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RESULT 12
US-09-438-486-173
; Sequence 173, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY:
LOCATION: 1..4029
OTHER INFORMATION: /note="preliminary sequence for
OTHER INFORMATION: human trf cdna insert of
OTHER INFORMATION: plasmid pGRN121"
US-09-438-486-173

Query Match 95.7%; Score 3832.6; DB 9; Length 4029;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;

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QY 8 GCAGCGCTGCGTCTGCTGCGCAGCTGGGGAAGCCCTGGCCCCCGCCGATGCC 67
Db 1 GCAGCGCTGCTGCTGCTGCGCAGCTGGGGAAGCCCTGGCCCCCGCCGATGCC 60
QY 68 GCGCGCTCCCGCGCTGCGAGCCGCTGCTGCTGCGCAGCCACTACCGCAGGTGCT 127
Db 61 GCGCGCTCCCGCGCTGCGAGCCGCTGCTGCTGCGCAGCCACTACCGCAGGTGCT 120
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RESULT 13
US-10-053-758-173
Sequence 173, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

FEATURE:
NAME/KEY: LOCATION: 1..4029
OTHER INFORMATION: /note="preliminary sequence for
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US-10-053-758-173

Query Match 95.7%; Score 3832.6; DB 9; Length 4029;
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Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;

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Db 2573 CTGCAGCTGTGCTACGGCGCAGATGGAAGAACAAAGCTGTTTGGCGGGATTCGGCGGAGCG 2632
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QY 2729 GAAGACAGTGTGAACCTTCCCTGTGAAGACGAGGCCCTGGGTGGCAAGGCTTTGTGTA 2788
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QY 3209 CGCCGGCCCTCTGCCCCCTCCGAGAGCCGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAA 3268
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QY 3569 CTGATGTCCGGCTGAGAGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3628
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QY 3629 GCTGAGTGTCCAGACACACCTGCGCTTTCACCTCCCAACAGGCTGGCGCTGCGCTCCACC 3688
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QY 3929 GGGGAGGTGCTGTGGAGTAAATATGATGATGATTTTTCAGTGTGTAAGAAAAAAA 3988
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QY 3989 AAAAAAAAAAAAAAAAAA 4005
Db 4013 AAAAAAAAAAAAAAAAAA 4029

RESULT 14
US-10-054-295-173
; Sequence 173, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: LOCATION: 1..4029
; OTHER INFORMATION: /note= "preliminary sequence for
; human TRT cDNA insert of
; plasmid pGRN121"
; SEQUENCE DESCRIPTION: SEQ ID NO: 173:
; US-10-054-295-173
Query Match 95.7%; Score 3832.6; DB 9; Length 4029;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;
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QY 188 GGACCGGCGGCTTTCGCGGCGCTGTGCGGCAAGTGCCTGTGCTGGGAGCTGGAGCC 247
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QY 308 CCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGGCGGAAGAACGTGCTGGCTTGGCTTGGC 367

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Db 361 GCTGTGACGGGGCGCGGGGGCCCCCGAGGCTTACACACAGCGTGGCAGCTA 420
QY 428 CCTGCCAACACAGGTGACCGACGACACTGCGGGGAGCGGGCGTGGGGCTGCTGTCG 487
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Db 421 CCTGCCAACACAGGTGACCGACGACACTGCGGGGAGCGGGCGTGGGGCTGCTGTCG 480
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QY 548 GCGTCCACGCTGCGCTTACAGGTGTGCGGGCGCGCTGTACCAGCTCGGCGCTGCCAC 607
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QY 608 TCAGGGCGGGCGCGCGCGCACACGCTAGTGACCGCGAAGCGCTGGGATGGAACGGGC 667
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Db 898 CACCTCTTGGAGGTTGCGTCTGTGGACGCGCCACTCCACCACATCCGTGGCGGCCA 957
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Db 1017 CCGGTTACCGCGGAGACCAAGCACTTCTTACTCTCAGGGCACAAGNA--CACTGCG 1074
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Db 2393 GGANAACAGGCGCGTGAAGGATGCCGTGCTATCGAGCAGAGCTCCTCCTGAATGAGGC 2452
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; Sequence 173, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morlin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-Oct-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY:
LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary sequence for
human TRT cDNA insert of
plasmid pGRN121"
SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-10-054-611-173

Query Match 95.7%; Score 3832.6; DB 9; Length 4029;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 3951; Conservative 0; Mismatches 39; Indels 47; Gaps 11;
QY 8 GCAGCGCTGCGTCTCTGCGCAGCGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCC 67
DB 1 GCAGCGCTGCGTCTCTGCGCAGCGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGCAGCGTGGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGCT 127
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DB 1433 GTACGGCTTGTGCGGG 1492
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Job time : 1537 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2003, 15:16:54 ; Search time 5223 Seconds
(without alignments)
12421.811 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: em_estin:*
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5: em_estov:*
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7: em_estro:*
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11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	765.2	19.1	925	13	BM453198 AGENCOURT
2	465.4	11.6	468	10	BM270031 xv57e03.x
3	445	11.1	492	14	BM824748 K-EST0096
4	430.8	10.8	851	13	BG917907 602820830
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6	385.8	9.6	389	9	AA281296 zt08g02.r

7	362.8	9.1	664	14	BQ258274 NISC_Kp11
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10	292.8	7.3	614	10	BB651920 BB651920
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12	276.2	6.9	866	10	BE371943 601217728
13	273.4	6.8	715	10	BE396925 601290610
14	270.6	6.8	679	10	BE396606 601289077
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16	265.8	6.6	610	10	BE514188 601316376
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18	246.2	6.1	779	10	BE268183 601125261
19	192.2	4.8	3783	11	BC030829 Homo sapi
20	188.6	4.7	347	10	AW244516 BR_END06B
21	187.4	4.7	3210	11	BC017493 Homo sapi
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ALIGNMENTS

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VERSION BM453198.1 GI:18502238
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM12208 row: p column: 01
High quality sequence stop: 646.
location/Qualifiers
1. 925

FEATURES
source

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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
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ORIGIN

Query Match      19.1%; Score 765.2; DB 13; Length 925;
Best Local Similarity 76.9%; Pred. No. 3.3e-59;
Matches 821; Conservative 0; Mismatches 30; Indels 216; Gaps 4;

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QY 2946 CTCTTGGGGTCTTGGGCTGAAGTGTACAGCCCTGTTCTGTGATTGACAGGTGAACAGC 3005
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Db 857 ----- 856
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RESULT 2
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VERSION AM270031.1
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE 1 (bases 1 to 468)
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 416.
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1. 468
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2817244"
/tissue_lib="NCI_CGAP_Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
BASE COUNT      100 a      137 c      144 g      86 t      1 others
ORIGIN

Query Match      11.6%; Score 465.4; DB 10; Length 468;
Best Local Similarity 99.6%; Pred. No. 1.5e-32;
Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3514 CACCCAGGCGCCACCGCTGGAGTGTGAGGCCCTGAGTGTGTTGGCCGAGGCTGCA 3573
Db      468 CACCCAGGCGCCACCGCTGGAGTGTGAGGCCCTGAGTGTGTTGGCCGAGGCTGCA 409
QY 3574 TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCAAGGGCTGA 3633
Db      408 TGTCCGGTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCAAGGGCTGA 349
QY 3634 GTGTCCAGACACCTGCGCTTTCATCTCCACAGGCTGGCGCTCGGCTCCACCCAGC 3693
```

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Db 348 GTGTCCAGCACACCTGCCGTTTCACTTCNCACACAGGCTGGCGCTCGCTCCACCCGAGG 289
QY 3694 GCCAGCTTTTCCCTCACCAGGAGCCCGGCTTCCACTCCCAACATAGGAATAGTCCATCCCC 3753
Db 288 GCCAGCTTTTCCCTCACCAGGAGCCCGGCTTCCACTCCCAACATAGGAATAGTCCATCCCC 229
QY 3754 AGATTCGCCATTTGTTCACCCCTCGCCCTGCTTGCCTTTCACCCCAACATAGTCCAG 3813
Db 228 AGATTCGCCATTTGTTCACCCCTCGCCCTGCTTGCCTTTCACCCCAACATAGTCCAG 169
QY 3814 GTGAGAGACCCGTGAGAAGGAGACCCCTGGAGCTCTGGAAATTGGAGTGACCAAAAGGTGCCC 3873
Db 168 GTGAGAGACCCGTGAGAAGGAGACCCCTGGAGCTCTGGAAATTGGAGTGACCAAAAGGTGCCC 109
QY 3874 CTGTACACAGCGGAGGAGACCCCTGCACCTGGATGGGGGTCCCTGTGGTCAAAATTGGGGGGA 3933
Db 108 CTGTACACAGCGGAGGAGACCCCTGCACCTGGATGGGGGTCCCTGTGGTCAAAATTGGGGGGA 49
QY 3934 GGTCCTGTGGAGTAAATATCTGATATATAGTTTTTCAGTTTGA 3981
Db 48 GGTCCTGTGGAGTAAATATCTGATATATAGTTTTTCAGTTTGA 1

RESULT 3
BM824748 492 bp mRNA linear EST 06-MAR-2002
LOCUS R-EST0096335 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-99-E07
DEFINITION 5', mRNA sequence.
ACCESSION BM824748
VERSION BM824748.1 GI:19181161
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 492)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
Plate: 99 row: E column: 07
High quality sequence stop: 492.
location/Qualifiers
1..492
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNU16n1-99-E07"
/clone_lib="S22SNU16n1"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcorI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldio, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

BASE COUNT 96 a 152 c 131 g 113 t
ORIGIN
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Query Match 11.1%; Score 445; DB 14; Length 492;
Best Local Similarity 100.0%; Pred. No. 9.4e-31;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2739 GTGAACCTCCCTGTAGAGACGAGGCGCTGGTGACAGGCTTTTGTTCAGATGCCGGCC 2798
Db 1 GTGAACCTCCCTGTAGAGACGAGGCGCTGGTGACAGGCTTTTGTTCAGATGCCGGCC 60
QY 2799 CACGGCCTATTCCCTGGTGCGGCGCTGCTGTGATACCCGACCCCTGAGGTGCAGAGC 2858
Db 61 CACGGCCTATTCCCTGGTGCGGCGCTGCTGTGATACCCGACCCCTGAGGTGCAGAGC 120
QY 2859 GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTACCTTCAACCGCGCTTC 2918
Db 121 GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTACCTTCAACCGCGCTTC 180
QY 2919 AAGGCTGGAGGAACATGCGTCGCAAACTCTTGGGCTCTTGGCGCTGAAGTGTACAGC 2978
Db 181 AAGGCTGGAGGAACATGCGTCGCAAACTCTTGGGCTCTTGGCGCTGAAGTGTACAGC 240
QY 2979 CTGTTTCTGGAATTTGCAAGGTGAACAGCCTCCAGAGGCTGTGCAACCAACATCTACAAGATC 3038
Db 241 CTGTTTCTGGAATTTGCAAGGTGAACAGCCTCCAGAGGCTGTGCAACCAACATCTACAAGATC 300
QY 3039 CTCCTGCTCCAGGCGGTACAGGTTTTCACGCGATGTGTGCTGACGCTCCCATTTTCATCAGCAA 3098
Db 301 CTCCTGCTCCAGGCGGTACAGGTTTTCACGCGATGTGTGCTGACGCTCCCATTTTCATCAGCAA 360
QY 3099 GTTTGGAAGAACCCCGACATTTTTCCTGCGCGTCATCTGTGACACGGCCCTCTGCTAC 3158
Db 361 GTTTGGAAGAACCCCGACATTTTTCCTGCGCGTCATCTGTGACACGGCCCTCTGCTAC 420
QY 3159 TCCATCCTGAAGCCAGAACGCGAG 3183
Db 421 TCCATCCTGAAGCCAGAACGCGAG 445

RESULT 4
BG917907 851 bp mRNA linear EST 05-JUN-2001
LOCUS 602820830F1 NCL_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
DEFINITION mRNA sequence.
ACCESSION BG917907.1 GI:14298383
VERSION BG917907
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA library Preparation: Life Technologies, Inc.
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10903 row: K column: 08
High quality sequence stop: 753.
location/Qualifiers
1..851
source
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4949887"
/clone_lib="NCL_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
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/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 184 a 238 c 214 g 215 t
ORIGIN

Query Match 10.8%; Score 430.8; DB 13; Length 851;
Best Local Similarity 20.1%; Pred. No. 1.7e-29;
Matches 597; Conservative 0; Mismatches 227; Indels 2145; Gaps 3;

QY 458 GGGAGCGGGGCTGGGGCTCTGCTGCCCGCGTGGGCGACGAGCTGCTGTTCACT 517
| | | | | | | | | | | | | | | | | |
Db 8 GTGGGTGCAGCGGGATGGGTCTTTACG----- 37
QY 518 GCTGGCAGCTGCGGCTTTGTGTGTGTGCTCCAGCTGCGCTACCAAGTGTGCGG 577
38 ----- 37
QY 578 GCCCGCGCTGACAGCTCGCGCTGCCACTAGCGCCCGCCCGCACAGCTAGTGG 637
38 ----- 37
QY 638 ACCCCGAAGCGTCTGGGATGCGAACGGCCGTGAACCATAGCGTACGGAGCGCGGGGT 697
38 ----- 37
QY 698 CCCCCGCGCTGCCAGCCCCCGGTGCGAGAGCGCGGGGGCAGTGCACCGAAGTCT 757
38 ----- 37
QY 758 GCCGTGCCCCAAGAGGCCCGCGCTGGCGCTGCCCTGAGCCGGAGCGAGCGCCGTTGG 817
38 ----- 37
QY 818 GCAGGGGTCTGGGCCCAACCGGGCAGAGCGCGTGGACCGAGTGAACCGTTTCTGTGT 877
38 ----- 37
QY 878 GGTGTCACTGCCAGACCCCGCGAAGAAGCACTCTTTGGAGGGTGGCTCTCTGGCAC 937
38 ----- 37
QY 938 GCGCCACTCCCAACCATCCGTGGGGCCCAAGCACACGGGGCCCCCATCCACATCGCG 997
38 ----- 37
QY 998 GCCACCAAGTCCCTGGGACACGCCCTTGTCCCGGGGTAGCGCCGAGACCAAGCACTTCT 1057
38 ----- 37
QY 1058 CTACTCCTCAGGAGACAAGAGAGAGCTGGGCCCTCTTCTACTCAGCTCTGTAGGCC 1117
38 ----- 37
QY 1118 CAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCATTTTCTGGTTCAGGCCCTGGAT 1177
38 ----- 37
QY 1178 GCCAGGAGCTCCCGCAGGTTGCCCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCT 1237
38 ----- 37
QY 1238 GTTCTGAGCTGCTTGGGAACACGCGCAGTGCCCCCTACGGGGTGTCTCTCAAGACGCA 1297
38 ----- 37
QY 1298 CTGCCCCGTGCGAGCTGCGGTACCCCCAGACGCGGGTGTCTGTGCCCGGAGAAACCCCA 1357
38 ----- 37

QY 1358 GGGCTCTGTGGCGGGCCCCCGAGGAGGAGACACAGACCCCCGTCGCCCTGTGACGTGCT 1417
38 ----- 37
QY 1418 CCGCCAGCACAGACGCCCCCTGGCAGGTGTACGGCTTGTGCGGGCTGCTGCGCGGCT 1477
38 ----- 37
QY 1478 GGTCCCCCAGGCGCTGTGGGGCTCCAGGCACACAAGACCGCGCTTCTCAGGAACACCAA 1537
38 ----- 37
QY 1538 GAAGTTCATCTCCCTGGGGAAGCATGCAAGCTCTCGCTGCAGAGAGCTGAGTGAAGAT 1597
38 ----- 37
QY 1598 GAGCGTGGGAGCTGCGCTTGGCTGCGCAGAGAGCCAGGGGTTGGCTGTCTCCGGCCGC 1657
38 ----- 37
QY 1658 AGAGCACCGTCTGCTGAGAGATCTTGCCCAAGTTCTTGCACCTGGCTGATGATGTGTA 1717
38 ----- 37
QY 1718 CGTCTGAGCTGCTCAGCTCTTTCTTTATGTACGGAGACACAGCTTCAAAAGAACAG 1777
38 ----- 37
QY 1778 GCTCTTTTCTACCGAAGAGTGTCTGAGCAAGTTGCAAGCATTGAATCAGACAGCA 1837
38 ----- 37
QY 1838 CTTGAAGAGGTGCAGCTCGGGAGCTGTGGAAGCAGAGTCAAGCATCGGGAAGC 1897
38 ----- 37
QY 1898 CAGGCCCCCTGCTGACGTCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCC 1957
38 ----- 37
QY 1958 GATTGTGAACATGACTACGTGTGGAGCCAGAACGTTCCGACAGAGAAAAGGGCCGA 2017
38 ----- 37
QY 2018 GCCTCTCACTGAGGGTGAAGGACACTGTTACGCTGTCTCACTACGAGCGGGCGCGG 2077
38 ----- 37
QY 2078 CCCCCGCTCCTGGGGCCTCTGTGTGGGCTGAGCATATCCACAGGGCCTGGCGCAC 2137
38 ----- 37
QY 2138 CTTCGTGCTGCTGTGGGGCCAGAGACCGCGCCTGAGCTGTACATCCCCAGAGACAG 2197
38 ----- 37
QY 2198 GCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGGGTA 2257
38 ----- 37
QY 2258 TGCCGTGTCAGAGGCCCGCCATGGGACGTCGCCAAGGCTTCAAGAGCCACGCTCTC 2317
38 ----- 37
QY 2318 TACCTGACAGACCTCCAGCCGTACATGCGAGAGTTGCTGCTCACCCTGCAGAGACAG 2377
38 ----- 37
QY 2378 CCGCGTGAAGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGG 2437
38 ----- 37
QY 2438 CCTCTGACGCTCTCTACGCTTCATGTGCCACACGCCGCTGGCATCAGGGGCAAGTC 2497

Db	38	-----	37
QY	2498	CTACGTCAGTGCAGGGATCCGACGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCT	2557
Db	38	-----	37
QY	2558	GTGCTACGGGCACATGAGAGACAAGCTGTTTGGGGGATTCGGCGGAGCGGGCTGCTCCT	2617
Db	38	-----	37
QY	2618	GCCTTTGATGATGATTTCTTGTGTGACACCTCCTCACCACCGGAAACCTTCT	2677
Db	38	-----TTGTGTGATGACTTCTGTAGGTGACGCCCTCACTTGACCAAGCAAAAACCTTCT	93
QY	2678	CAGGACCCCTGTCGAGGTGTCCTGAGTATGGCTGGCTGGTGAAGTTCGGGAGACAGT	2737
Db	94	CAGCACCCCTGGTCCATGGGGTCTCCTGAGTATGGGTGATGATAAAGTTCGAGAGACAGT	153
QY	2738	GGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCAGCGCTTTGTTCAGATGCCGGC	2797
Db	154	GGTGAACCTTCCCTGTGAGACCTGTACCTGGGTGGTGGCAGCTCCATACAGCTGCTGC	213
QY	2798	CCACGGCCTATTCCTCCCTGCTGCGGCTGCTGCTGATACCCGGACCTGGAGTGCAGAG	2857
Db	214	TCACTGCTGTTTCCCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	273
QY	2858	CGACTACTCCAGCTATGCGCCGAGCCTCATCAGAGCAGTCTCACCCTTCAACCGGGCTT	2917
Db	274	TGACTACTCAGGTATGCGCCAGACCTCAATTAAGACGAGCCTCACCCTTCCAGAGTGTCT	333
QY	2918	CAAGGCTGGAGGAGAACATGCGTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGTGTACAG	2977
Db	334	CAAAAGCTGGAGAGACCATGCGGAGAACAGCTCCTGTCGGTCTTGGCGTGAAGTGTACCG	393
QY	2978	CCTGTTTCTGGATTTGACAGGTGAACAGCGCTCCAGACGCTGTGCACCAACATCTACAAGAT	3037
Db	394	TCTATTTCTAGACTTGTGAGGTGAACAGCGCTCCAGACAGTCTGCATCAATATATACAAGAT	453
QY	3038	CCTCCTGCTGAGGCGGTACAGGTTTTCAGCGCATGTGCTGACGCTCCCATTTTCATCAGCA	3097
Db	454	CTTCCTGCTTACAGGCTTACAGGTTCCATGATGTGATTCAGCTTCCCTTTGACCAAGCG	513
QY	3098	AGTTTGAAGAACCACATTTTTCCTCGCGCTCATCTCTGACACGGCTCCCTGTGCTA	3157
Db	514	TGTTAGGAAGAACTCACATTTCTTCTGGGCTATCTCCAGCAAGCATTCCTGTGCTA	573
QY	3158	CTCCATCCTGAAAGCAAGCAAGGATGCTGCTGGGGGCAAGGGCCGCCGCCGCC	3217
Db	574	TGCTATCTCTGAGGTCAAGAAATCCAGGAATGACACTAAAGGCCCTGTGGCTC-----	624
QY	3218	TCTGCCCTCCGAGGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3276
Db	625	-CTTCTCTCTGAAAGCCGACATTTGGCTCTGCTACCAAGCCCTTCCGTGCTCAAGCTGGCTG	683
QY	3277	GACACCGTGTACCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3336
Db	684	CTCATTTCTGTATCTACAAATGTCTCTGCGGACCTGTGAGGACAGCCCAAAAACCGCTGT	743
QY	3337	GTGCGAAGCTTCCCGGGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3396
Db	744	GCCGGAAGCTGCGAGAGGCGACATGACCATGCTTACAGCTGCAGCTGACCCAGACCTAA	803
QY	3397	CCTCAGACTTCAAGACCATCTCTGACTGA	3425
Db	804	GGACAGACTTTCAGGACCATTTGGACTAA	832

RESULT 5
AM276315/c 416 bp mRNA linear EST 03-JAN-2000
LOCUS xrl0b12.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3',
DEFINITION mRNA sequence.

ACCESSION	AM276315	
VERSION	AM276315.1	
KEYWORDS	GI:6663345	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 416)	
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html Seq primer: -40UP from Gibco High quality sequence stop: 413. Location/Qualifiers 1. 416 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2759711" /clone_lib="NCI-CGAP_Lu28" /tissue_type="two pooled squamous cell carcinomas" /lab_host="DH10B" /note="Organ: Lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."	
BASE COUNT	90 a 118 c 130 g 78 t	
ORIGIN		
Query Match	10.4%; Score 416; DB 10; Length 416;	
Best Local Similarity	100.0%; Pred. No. 3.6e-28;	
Matches	416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	3565 AGGCTGCATGTCGCGCTGAAGGCTGAGTGTCCGGCTGAGGAGTGTCCAGCC	3624
Db	416 AGGCTGCATGTCGCGCTGAAGGCTGAGTGTCCGGCTGAGGAGTGTCCAGCC	357
QY	3625 AAGGCTGAGTGTCCAGCACACCTGCGCTTTCACCTTCCACACAGGCTGGCGCTC	3684
Db	356 AAGGCTGAGTGTCCAGCACACCTGCGCTTTCACCTTCCACACAGGCTGGCGCTC	297
QY	3685 CACCCAGGGCCAGCTTTTCTCACCAGGAGCGCGGCTTCCACTCCCCACATAGGAATAG	3744
Db	296 CACCCAGGGCCAGCTTTTCTCACCAGGAGCGCGGCTTCCACTCCCCACATAGGAATAG	237
QY	3745 TCCATCCCCAGATTGCGCATTTGTTACCCCGCTGCGCTCTTGGCTTCCACCC	3804
Db	236 TCCATCCCCAGATTGCGCATTTGTTACCCCGCTGCGCTCTTGGCTTCCACCC	177
QY	3805 ACCATCCAGGTGAGACCCCTGAGAAAGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCA	3864
Db	176 ACCATCCAGGTGAGACCCCTGAGAAAGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCA	117
QY	3865 AGGTGTCCCTGTACACAGGCGAGGACCCCTGACCTGTGATGGGGTCCCTGTGGGTCAA	3924
Db	116 AGGTGTCCCTGTACACAGGCGAGGACCCCTGACCTGTGATGGGGTCCCTGTGGGTCAA	57
QY	3925 TTGGGGGAGGTGCTGTGGGAGTAATAATATATATAGTTTTCAGTTTGA	3980
Db	56 TTGGGGGAGGTGCTGTGGGAGTAATAATATATATAGTTTTCAGTTTGA	1

RESULT 6
AA281296

RESULT 6
AA281296

LOCUS AA281296 389 bp mRNA linear EST 14-AUG-1997
DEFINITION zt08g02.r1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:712562 5',
mRNA sequence.
ACCESSION AA281296
VERSION AA281296.1 GI:1924194
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 389)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2187 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 385.
FEATURES
source
1. 389
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:712562"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT7R3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dt) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTT-3',
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7R3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaudo."

BASE COUNT 87 a 102 c 123 g 77 t
ORIGIN

Query Match 9.6%; Score 385.8; DB 9; Length 389;
Best Local Similarity 99.5%; Pred. No. 1.7e-25;
Matches 387; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1686 GCCAAGTTCCTGCACCTGGCTGATGAGTGTAGCTGCTGCAGCTGCTCTTCTT 1745
DB 1 GCCAAGTTCCTGCACCTGGCTGATGAGTGTAGCTGCTGCAGCTGCTCTTCTT 60
OY 1746 TATGTCACGAGACCAACGTTTCAAAAGACAGGCTCTTTTCTACCGAAGAGTGTCTGG 1805
DB 61 TATGTCACGAGACCAACGTTTCAAAAGACAGGCTCTTTTCTACCGAAGAGTGTCTGG 120
OY 1806 AGCAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGCTGCAGCTCGGGAGCTG 1865
DB 121 AGCAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGCTGCAGCTCGGGAGCTG 180
OY 1866 TCGGAAGCAGAGGTCAGGACGATCGGGAAGCCAGGCCGCCCTGCTGACGCTCCAGACTC 1925
DB 181 TCGGAAGCAGAGGTCAGGACGATCGGGAAGCCAGGCCGCCCTGCTGACGCTCCAGACTC 240
OY 1926 CGCTTCATCCCAAGCCTGACGGGCTGCGCCGATTGTGAACATGAGTACGTCTGGGA 1985
DB 241 CGCTTCATCCCAAGCCTGACGGGCTGCGCCGATTGTGAACATGAGTACGTCTGGGA 300
OY 1986 GCCAGAACGTTCCGACAGAGAAAGAGGCGGAGCGTCTCACCCTGAGGCTGAAGGCACTG 2045
DB 301 GCCAGAACGTTCCGACAGAGAAAGAGGCGGAGCGTCTCACCCTGAGGCTGAAGGCACTG 360

OY 2046 TTCAGCGTGTCTCACTACGAGCGGCGCG 2074
DB 361 TTCAGCGTGTCTCACTACGAGCGGCGCG 389

RESULT 7
LOCUS BQ258274 664 bp mRNA linear * EST 06-MAY-2002
DEFINITION NISC_kp11g04.q3 Baker mouse embryo e7.5 Mus musculus CDNA clone
IMAGE:5409222, mRNA sequence.
ACCESSION BQ258274
VERSION BQ258274.1 GI:20459030
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 664)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: J. Baker (Stanford University)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNLN
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
info@image.llnl.gov
MGI:1845958

FEATURES
source
1. 664
/organism="Mus musculus"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:5409222"
/clone_lib="Baker mouse embryo e7.5"
/tissue_type="embryo, late gastrula"
/dev_stage="embryo, 7.5 dpc"
/lab_host="XL1-Blue"
/note="Vector: pCS105; Site_1: NotI; Site_2: SalI; cDNA
made by oligo-dT priming. Directionally cloned into
SalI/NotI sites using the following 5' adaptor:
5'-TCGACCCACGCGTCCG-3'. Size-selected for average insert
size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
University)."
BASE COUNT 155 a 177 c 183 g 149 t
ORIGIN

Query Match 9.1%; Score 362.8; DB 14; Length 664;
Best Local Similarity 68.3%; Pred. No. 1.9e-23;
Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;

OY 1115 GCCCAGCCTGACTGGCGCTCGGAGGCTCGTGAGAGACCATCTTTCGTGGTTCAGGCCCTG 1174
DB 9 GCCTAAGTTCAGTGGGGCCAGGAGACTGTGAGATCATCTTTCGTGGCTCAAGGCTAG 68
OY 1175 GATGCCAGGACTCCCGCAGGTGCCCCGCTGCCAGCGCTACTGCGCAATGCGGCC 1234
DB 69 GACATCAGAGCACTCTGCAGACACACCGCTATCGCGTGAATCTGCGAGATGCGGCC 128
OY 1235 CCTGTTTCGAGCTGCTTGGGAACACGCGCAGTGGCCCTACAGGGTGTCTCTCAAGAC 1294
DB 129 CCTGTTTCACAGCTGTGTGAACCATGAGAGTGCCAAATATGTGAGACTCCTCAGGTC 188
OY 1295 GCACTGCCCGCTGCGAGCTGCGGTACCCACGACGCGGCTGTCTGTGCCCGGAGAAGCC 1354
DB 189 ACATTGCAGGTTTCGAACAGCAACACCAACAGGTGACAGATGCTT----- 232

OY 1355 CCAGGGCTCTGTGGGCCCCGAGAGGAGACAGACACCCTCGCCTGTGTCAGCT 1414
Db 233 -----TGAAACACAGCCACCCGACACCTCAHGGATT 263
OY 1415 GCTCCGGCACAGACAGACCCCTGGAGGTGTACGGCTTCGTGGGGCCTGCTGCGCCG 1474
Db 264 GCTCCGGCTGCACAGACAGCTCCCTGGCAGGTATATGTTTCTTGGGGCCTGTCTCTGCAA 323
OY 1475 GCTGTGCCCCAGGCTCTGGGGCTCCAGGACACAGAACGCCCTTCTCAGGAACAC 1534
Db 324 GGTGTGTCTGTAGTCTCTGGGGTACCAAGCACAAATGAGCGCGCCTTCTTAAGAACTT 383
OY 1535 CAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTGCTGCAGAGAGCTGACGTGAA 1594
Db 384 AAAGAAGTTCATCTCGTTGGGAAATACGGCAAGCTATCACTGCAGGAACGTGATGTGAA 443
OY 1595 GATGAGCGTCGGGAGCTGCGCTTGGCTGCGCAGAGACCCAGGGGCTTGGCTGTGTCGGC 1654
Db 444 GATGAAGTAGAGAGATTGCCACTGGCTCCCGACAGACCCAGGAAGACCGTGTCCCGCCG 503
OY 1655 CGCAGAGACCGCTGCGGTGAGAGAGATCCCTGCGCAAGTTCCCTGCACTGGCTGATGAGTGT 1714
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OY 1715 GTACGTGCTGAGCTGCTCAGGTCCTTTCTTTATGTCAAGAGACCAAGTTCAAAAGAA 1774
Db 564 ATACGTGTACAGCTGCTTAGGTGATCTTTTACATCACAGAGAGACATTCAGAAAGAA 623
OY 1775 CAGGCTCTTTTCTACCGGAAGAGTGTCTGAGCAAGTTGC 1815
Db 624 CAGGCTCTTCTTCTACCGTAAGAGTGTGTGAGCAAGCTGC 664

RESULT 8
LOCUS BB618671 599 bp mRNA linear EST 26-OCT-2001
DEFINITION BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus
CDNA clone 5730412M20 5', mRNA sequence.
ACCESSION BB618671
VERSION BB618671.1 GI:16458173
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 599)
REFERENCE
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
, Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
, D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscl.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki,Y.
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamataka,I., Aizawa
, K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
source
1..599
/organism="Mus musculus"
/strain="C57BL/6J"
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/dev_stage="8 days embryo"
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCACAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of subtraction to
Rot = 100.0 Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATTCGAGTTAATTAAATTAATCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI."
BASE COUNT 91 a 185 c 181 g 142 t
ORIGIN
Query Match 8.0%; Score 322; DB 10; Length 599;
Best Local Similarity 74.9%; Pred. No. 7.9e-20;
Matches 403; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
OY 9 CAGCGCTGCGTCTGCTGCGACGTGGGAAGCCCTGGCCCCGACCCCGGATGCCG 68
Db 61 CACCCTTGCACTGTGTGTTCCCGACAGTGGAGGCCCATGCCGCTTGAGCACAAATGACC 120
OY 69 CGCGCTCCCGCTGCGCGAGCCGCTGCTGCTGCGAGCCACATACCGCGAGTGTCTG 128
Db 121 CGCGCTCCTCGTTCGCCCGCGGCTGCTGCTGCGAGCCGATACCGGGAGGTGTGG 180
OY 129 CCGCTGGCCACGTTGCTGGGGGCTGGGGCCAGGGCTGGGGCGGCTGTGCAGCGGGG 188
Db 181 CCGCTGGCAACCTTTGTGGGGGCTGGGGCCGAGGGCAGCGGCTGTGTCAACCCGGG 240
OY 189 GACCGCGCGGCTTCCGCGCGCTGTGTGGCCAGTGCCTGTGTGCTGCCCTGGGAGCA 248
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OY 249 CGGCGGCCCCCGCGGCGCCCTTCCTCCGCAAGTGTCTGCTGCTGAAGAGAGTGTGGCC 308
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1 11 1111111 11 11111111 11 11 1111111111 11 11111 11

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Db      361 AGGTTGTGACAGACTCTGCGAGCGCAACGAGAGAAACGTGCTGGCTTTTGCTTGAG 420
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Db      421 CTGCTTAACGAGGCCAGAGAGCGGGCCCTCCATGGCCTTCACTAGTAGCGCTAGCTAC 480
QY      429 CTGCCCCAACACGCTGACCGACGACCTGCGGGGGAGCGGGGCGTGGGGCTGCTGCGC 488
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Db      481 TTGCCCAACACTGTTATTGAGACCTGCTGTCAGTGTGATGATGCTACTGTTGAG 540
QY      489 CGCGTGGGCGACGCTGCTGTTACCTGCTGCGACGCTGCGGCTCTTGTGCTGG 546
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RESULT 9
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LOCUS   AA811084 340 bp mRNA linear EST_19-FEB-1998
DEFINITION oa85c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319048 3',
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ACCESSION AA811084
VERSION   AA811084.1 GI:2880695
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 340)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert length: 2249 Std Error: 0.00
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                was prepared from human tonsillar cells enriched for
                germinal center B cells by flow sorting (CD20+, IgD-),
                provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                primed with a Not I - oligo(dt) primer
                [5'-TGTACCAATCGAAGTGGAGGCGCGCCCTCATTTTCTTTTCTTTT-3'
                ]. Double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. Library
                went through one round of normalization, and was
                constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 73 a 86 c 100 g 81 t
ORIGIN
Query Match 7.9%; Score 318.4; DB 9; length 340;
Best Local Similarity 99.18; Pred. No. 1.7e-19;
Matches 339; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Db      340 TCAC TTCACAGAGG-TGGCGCTCGGCTCCACCCAGGGCAGCTTTCTCCACAGAG 282
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Db      281 CCGGCTTCACACTCCACATAGGAATAGTCCATCCCCAGATTCGCCATGTTCACCCCT 222
QY      3776 CGCCCTGCCCTCTTGTGCTTCCACCCCAACCATCCAGGTGAGACCCCTGAGAAGACC 3835
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Db      221 CGCCCTGCCCTCTTGTGCTTCCACCCCAACCATCCAGGTGAGACCCCTGAGAAGACC 162
QY      3836 TGGAGCTCTGGGAATTGAGGTGACCAAGGTGCCCCGTGTACACAGGCGAGACCCTG 3895
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Db      161 TGGAGCTCTGGGAATTGAGGTGACCAAGGTGCCCCGTGTACACAGGCGAGACCCTG 102
QY      3896 CACCTGATGGGGGCTCCCTGTGGGTCAATTGGGGGAGGTGCTGTGGAGTAAATACT 3955
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RESULT 10
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LOCUS     BB651920
DEFINITION BB651920 RIKEN full-length enriched, ES cells Mus musculus cDNA
            clone C330020G14 5', mRNA sequence.
ACCESSION BB651920
VERSION   BB651920.1 GI:16486058
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 614)
AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
            Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
TITLE     Unpublished (2001)
JOURNAL   Contact: Yoshinide Hayashizaki
COMMENT   Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL: http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a

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RESULT 12
LOCUS BE371943 866 bp mRNA linear EST 21-JUL-2000
DEFINITION 601217728F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586614 5',
mRNA sequence.
ACCESSION BE371943
VERSION BE371943
KEYWORDS BE371943.1 GI:9317215
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 866)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM8748 row: h column: 07
High quality sequence stop: 639.

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/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: SalI;
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 157 a 231 c 253 g 225 t
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Query Match 6.9%; Score 276.2; DB 10; Length 866;
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Matches 474; Conservative 0; Mismatches 263; Indels 809; Gaps 4;

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QY 2677 TCAGAACCTTGCTCCGAGGTGCTCCCTGAGTATGCTGCGTGGTGAACCTTGGGAAGACAG 2736
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QY 2737 TGGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCAGCGCTTTGTTACAGATGCCG 2796
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QY 2797 CCCAGCGCTATTTCCCTGCTGGCGGCTGCTGCTGATACCGGACCCCTGGAGGTGACAG 2856
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QY 3217 C-----
Db 478 CTGGGTACTACATTTCTGTTTCTTCTTCTAGACACAGTGACCGGTGAGGCTGAAGTGA 537
QY 3218 -----TCTGCCCTCCGAGCGCGCTGACGTGGCTGTGCCACCAAGCATTTCTCTG 3263
Db 538 TAGAGGCCAAAGGTGTTCCCTTTCTTCATGAGATAGGATGGGACACTATGAGAGCATC 597
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QY 3324 CAGAGCAGCTGAGTCGGAAGTCCCGGGAGACGAGCTGACTGCCCTGGAGCGCAGCC 3383
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QY 3384 AACCCGGACTGCCCTCAGACTTCAAGACCATCTGAGTATGGCCACCGCCACAGC 3443
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QY 3444 CAGGCCGAGAGCAGACACAGACGCCCTGTACGCGCGGCTTACGTTCCAGGAGGAGAG 3503
Db 613 -----AGTCTCTGACAGACCATGGAG 634
QY 3504 GGGCGCCACACACAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCC 3563
Db 635 CCAAGGCCCTCCCTCTGTATGAGACTGGGACGGGATGGGGCTTGGTCTCTTACCTACC 694

QY 1079 GCAGCTGCGCCCTCTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGAG 1138
Db 318 ----- 317
QY 1139 GCTCGTGAGACCATCTTCTGCGTTCAGGCCCTGATGCCAGGACTCCCCAGGTT 1198
Db 318 ----- 317
QY 1199 GCGCCGCTGCCCCAGCGCTACTGGCAATGCGCCCCCTGTTCTGGAGCTGCTGGGA 1258
Db 318 ----- 317
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QY 1319 CACCCAGCAGCCGCTGTCTGTGCCCCGGAGAAGCCCGAGGCTCTGTGCGCGCCCCGA 1378
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QY 1439 GCAGGTGACGGCTTCGTGCGGGCTGCGCGCCGCTGCTGTCGCCAGGCCCTCTGGGG 1498
Db 318 ----- 342
QY 1499 CTCCAGGCACACGAACGCGCTCTCTCAGGAACACCAAGATTCTCTCTGGGAA 1558
Db 343 ATCTGATGTGGCATGTCTCTCTCTCTTA----- 371
QY 1559 GCATGCCAAGCTCTCGCTGACGAGAGCTGAGTGAAATGAGCGTGGGAGCTGCGCTTG 1618
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Db 372 ----- 416
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Db 417 GATCCTGGCCAACTTCTCTGCACTGGCTGATGAGTGTACGTCGTCAGCTGCTCAGGTC 476
QY 1739 TTTCTTT-TATGTACAGGAGACACAGTTCATAAAGAACAGGCTCTTTTCTACCGGAAGA 1797
Db 477 TTTCTTTATATGTACAGGAGACACAGTTCATAAAGAACAGGCTCTTTTCTACCGGAAGA 536
QY 1798 GTGTCTGAGCAAGTTGCAAGCATGTGAATCAGACGACACTTGAAGAGGCTGACGCTGC 1857
Db 537 GTGTCTGAGCAAGTTGCAAGCATGTGAATCAGACGACACTTGAAGAGGCTGACGCTGC 596
QY 1858 GGGAGCT-GTTCGGAAGCAGAGGTGAGGAGCATCGGG--AAGCCAGGCCCGCTGCTGA 1914
Db 597 GGGAGCTAGTCGGAAGCAGAGGTGAGGAGCATCGGGGAAGCCAGGCCCTGCTGCTGA 656
QY 1915 CGTCCAGACTCCGCTTCATCCCCCAAGCCTGACGGGCTGCGGC 1956
Db 657 CGTCCA---ACTCCGTTCATCCCAAGCTGAAGGGCTGCGGC 695

RESULT 14
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LOCUS 601289077F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619674 5',
DEFINITION mRNA sequence.
ACCESSION BE396606
VERSION BE396606.1 GI:9341882
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 679)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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High quality sequence stop: 656.
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 649)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 103 a 146 c 249 g 151 t
ORIGIN
Query Match 6.7%; Score 267.4; DB 10; Length 649;
Best Local Similarity 24.0%; Pred. No. 5.6e-15;
Matches 437; Conservative 0; Mismatches 166; Indels 1217; Gaps 7;
QY 119 CGAGTGTCTGCCGCTGGCCACAGTTCGTGCGGCGCTGGGGCCCGAGGCGCTGGCGGCTG 178
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SUMMARIES

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6	3982.6	99.4	4037	29	US-09-721-506-343	Sequence 343, App
7	3982.6	99.4	4038	13	US-08-974-524E-117	Sequence 117, App
8	3982.6	99.4	4038	13	US-08-974-584C-117	Sequence 117, App
9	3973.8	99.1	4023	13	US-09-026-981-35	Sequence 35, App
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DB 3781 CCAGATTCGCCATTTGTTCACCCCTGCGCCCTGCGCTTCTTGGCTTCCACCCCAACCATCC 3840
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DB 3841 AGGTGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
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DB 4021 AAAAAAAAAAAAAA 4035

RESULT 2
US-09-402-181A-343
Sequence 343, Application US/09402181A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181A
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of hTRT cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 343:
us-09-402-181a-343

Query Match 99.4%; Score 3982.6; DB 18; Length 4037;
Best Local Similarity 98.9%; Pred. No. 6.4e-140;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;

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RESULT 3
US-09-402-181B-343
; Sequence 343, Application US/09402181B
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lininger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"
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US-09-402-181B-343

Query Match 99.4%; Score 3982.6; DB 18; Length 4037;
Best Local Similarity 98.9%; Pred. No. 6.4e-140;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;

QY 8 GCAGCGTGCCTCTGTCGCACAGTGGGAAGCCCTGGCCCCCGGCCACCCCGCGATGCC 67
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Db 1 GCAGCGTGCCTCTGTCGCACAGTGGGAAGCCCTGGCCCCCGGCCACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGGACCCGCTGCGCTCCCTGCTGCGGACGCACTACCGCGAGTGCT 127
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Db 61 GCGCGCTCCCGCTGCGGACCCGCTGCGCTCCCTGCTGCGGACGCACTACCGCGAGTGCT 120
QY 128 GCCGCTGGCCAGTTCGTGCGGCGGCTGCGGCGCCCAAGGCTGGCGGCTGTGCGAGCGCG 187
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Db 121 GCCGCTGGCCAGTTCGTGCGGCGGCTGCGGCGCCCAAGGCTGGCGGCTGTGCGAGCGCG 180
QY 188 GGACCCCGGCGCTTCCGCGCGCTGTGCGCCAGTGCCTGTGCTGCTGCGCTGGGACGC 247
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Db 181 GGACCCCGGCGCTTCCGCGCGCTGTGCGCCAGTGCCTGTGCTGCTGCGCTGGGACGC 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCTTCCTCCGCGAGTGTCTGCTGAAGAGCTGTGGC 307
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Db 241 ACGGCGCGCGCGCGCGCGCGCGCTTCCTCCGCGAGTGTCTGCTGAAGAGCTGTGGC 300
QY 308 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGAAGACGTGTGCTGCGCTTCGCTGCG 367
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Db 301 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGAAGACGTGTGCTGCGCTTCGCTGCG 360
QY 368 GCTGCTGAGCGGGCGTA 427
|||||
Db 361 GCTGCTGAGCGGGCGTA 420
QY 428 CCG 487
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Db 421 CCG 480
QY 488 CCGCGTGGCGGACGACGTGCTGTTACCTGCTGCGACGCTGCGCGCTCTTGTGCTGCT 547
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Db 481 CCGCGTGGCGGACGACGTGCTGTTACCTGCTGCGACGCTGCGCGCTCTTGTGCTGCT 540
QY 548 GCGTCCAGCTGCGGCTACAGGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
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Db 541 GCGTCCAGCTGCGGCTACAGGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 608 TCAGGCG 667
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Db 601 TCAGGCG 660
QY 668 CTGGAACCATATGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 727
|||||
Db 661 CTGGAACCATATGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 720
QY 728 GAGGCG 787
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Db 721 GAGGCG 780
QY 788 TGCCCTGAGCGGAGCGGACCGCGGTTGGGCGAGGGGCTCTGGGCGCACCCGGGCGAGGAC 847
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Db 781 TGCCCTGAGCGGAGCGGACCGCGGTTGGGCGAGGGGCTCTGGGCGCACCCGGGCGAGGAC 840
QY 848 GCGTGGACCGAGTACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
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Db 841 GCGTGGACCGAGTACCGT 900
QY 908 CACCTCTTGGAGGGTGCCTCTGTGCGACGCGCGCACTCCACCCATCCGTTGGCGCGCA 967
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Db 901 CACCTCTTGGAGGGTGCCTCTGTGCGACGCGCGCACTCCACCCATCCGTTGGCGCGCA 960
QY 968 GCACACGCGGCG 1027
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Db 961 GCACACGCGGCG 1020
QY 1028 CCGGCTGTACGCGGAGACCAAGCACTCTCTACTCTCAGGCGACAGAGAGAGAGAGAGAG 1087
|||||
Db 1021 CCGGCTGTACGCGGAGACCAAGCACTCTCTACTCTCAGGCGACAGAGAGAGAGAGAGAG 1080

QY 1088 GCCCTCCTTCTACTACGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCGTGA 1147
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Db 1081 GCCCTCCTTCTACTACGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCGTGA 1140
QY 1148 GACCATCTTCTGGGTTCCAGGCGCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT 1207
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Db 1141 GACCATCTTCTGGGTTCCAGGCGCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCT 1200
QY 1208 GCCCAGCGCTACTGGCAATGCGGCCCTGTCTGTGAGCTGCTGGGAACCAACGCGCA 1267
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Db 1201 GCCCAGCGCTACTGGCAATGCGGCCCTGTCTGTGAGCTGCTGGGAACCAACGCGCA 1260
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Db 1261 GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCAACCCAGC 1320
QY 1328 AGCGGCTGTCTGTGCCCCGGGAGAACCCAGGGCTCTGTGGCGGCCCGCCGAGAGAGA 1387
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Db 1321 AGCGGCTGTCTGTGCCCCGGGAGAACCCAGGGCTCTGTGGCGGCCCGCCGAGAGAGA 1380
QY 1388 CACAGACCCCGCTGCGCTGTGAGCTGTCTCCGACAGACAGACCCCTTGCGAGGTGA 1447
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Db 1381 CACAGACCCCGCTGCGCTGTGAGCTGTCTCCGACAGACAGACCCCTTGCGAGGTGA 1440
QY 1448 CGGCTTCGTGGGGGCGCTGCGCTGCGCGCGCTGTGTCGCCAGGCTCTGGGGCTCCAGGCA 1507
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Db 1441 CGGCTTCGTGGGGGCGCTGCGCTGCGCGCGCTGTGTCGCCAGGCTCTGGGGCTCCAGGCA 1500
QY 1508 CAACGAACGCCGCTTCTCTCAAGAACACCAAGAGTTCACTCTCCCTGGGGAAGCATGCCAA 1567
|||||
Db 1501 CAACGAACGCCGCTTCTCTCAAGAACACCAAGAGTTCACTCTCCCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCTGAGAGAGCTGAGCTGGAAGATGAGCGTGGCGGACTGCGCTGGCTGGCGAG 1627
|||||
Db 1561 GCTCTGCTGAGAGAGCTGAGCTGGAAGATGAGCGTGGCGGACTGCGCTGGCTGGCGAG 1620
QY 1628 GAGCCAGGGGTTGGCTGTCTCCGCGCCGAGAGACACCGCTGCTGAGAGATCCTGGC 1687
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Db 1621 GAGCCAGGGGTTGGCTGTCTCCGCGCCGAGAGACACCGCTGCTGAGAGATCCTGGC 1680
QY 1688 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA 1747
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Db 1681 CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA 1740
QY 1748 TGTCAAGGAGACACAGTTTCAAAGAACAAGGCTCTTTTCTAACCGAAGAGTGTCTGAG 1807
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Db 1741 TGTCAAGGAGACACAGTTTCAAAGAACAAGGCTCTTTTCTAACCGGCGAGTGTCTGAG 1800
QY 1808 CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC 1867
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Db 1801 CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAGGCAAGCATGCGGAAGCCAGGCCCGCTGCTGAGCTCCAGACTCCG 1927
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QY 1923 CTTCATCCCCAAGCCTGACGGGCTGCGCGCGATTTGTAACATGACTACGTCTGGGAGC 1987
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Db 1921 CTTCATCCCCAAGCCTGACGGGCTGCGCGCGATTTGTAACATGACTACGTCTGGGAGC 1980
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Db 1981 CAGAAGCTTCCGAGAGAAAAGAGGCGCGAGCGTCTACCTCGAGGGGTGAAGGCACTGTT 2040
QY 2048 CAGCGTGTCACTACGAGCGGGGCGCGCGCGCGCGCTCTGGCGCGCTGTGTCTGGG 2107
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Db 2041 CAGCGTGTCACTACGAGCGGGGCGCGCGCGCGCGCGCTCTGGCGCGCTGTGTCTGGG 2100
QY 2108 CTTGAGCATATCCACAGGGGCTGGCGCACCTTCTGTGCTGCTGTGCGGGCCAGGACCC 2167
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Db 2101 CTTGAGCATATCCACAGGGGCTGGCGCACCTTCTGTGCTGCTGTGCGGGCCAGGACCC 2160
QY 2168 GCGGCTGAGCTGTA-----CATCCCCCA 2191

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Db 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACCAATCCCCCA 2220
QY 2192 GGACAGGCTCACGAGGTCACTCCGACATCATCAAAACCCAGAACAAGCATGCTGCGG 2251
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Db 2221 GGACAGGCTCACGAGGTCACTCCGACATCATCAAAACCCAGAACAAGCATGCTGCGG 2280
QY 2252 TCGTATGCCGTGTGCCAGAAAGCGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCA 2311
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Db 2281 TCGTATGCCGTGTGCCAGAAAGCGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCA 2340
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Db 2341 CGTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGGCTCACCTGAGGA 2400
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Db 2401 GACCAAGCCGCTGAGGGATGCCGTCTCATTCGAGCAGAGAGCTCTCCCTGAATGAGGCCAG 2460
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Db 2461 CAGTGGCTCTTGACAGCTCTTCTACGCTTCAATGTGTCACCAACGCGCTGCGCATCAGGG 2520
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QY 2852 GCAGAGGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2911
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Db 3001 TCACAGCCTGTTTCTGATTTGACGTTGAACAGCCTCCAGAGGTTGTGACCAACATCTA 3060
QY 3032 CAAGATCTCTCTGCTGACAGGCTTACAGGTTTACAGCATGTGTGCTGACGCTCCCATTTCA 3091
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Db 3061 CAAGATCTCTCTGCTGACAGGCTTACAGGTTTACAGCATGTGTGCTGACGCTCCCATTTCA 3120
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Db 3421 ACTGCCCTGAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA 3480
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QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGGGCT 3631
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QY 3632 GAGTGTCCAGACACCTGCGCTCTTCACTTCCACAGGCTGCGGCTCGGCTCCACCCCA 3691
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Db 3901 CCCTGTACACAGGCGAGAGCCCTGACCTGAGTGGGGTCCCTGTGGGTCAAAATTTGGGG 3960
QY 3932 GAGGTGCTGTGGGAGTAATACTGAATATATGAGTTTTCAGTTTGGAAAAA 3991
Db 3961 GAGGTGCTGTGGGAGTAATACTGAATATATGAGTTTTCAGTTTGGAAAAA 4020
QY 3992 AAAAAAAAAAAAAA 4006
Db 4021 AAAAAAAAAAAAAA 4035

RESULT 4
US-09-432-503-343
; Sequence 343, Application US/09432503.
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; ; NUMBER OF SEQUENCES: 727
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Townsend and Townsend and Crew LLP
; ; STREET: Two Embarcadero Center, Eighth Floor
; ; CITY: San Francisco
; ; STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 343:
; ; US-09-432-503-343
Query Match 99.4% Score 3982.6; DB 18; Length 4037;
Best Local Similarity 98.9% Pred. No. 6.4e-140;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;
QY 8 GCAAGCGCTGCTGCTGCTGCGACGCTGGGAAGCCCTGGCCCCGGCCAGCCCGCGATGCC 67
Db 1 GCAGGCGCTGCTGCTGCTGCGACGCTGGGAAGCCCTGGCCCCGGCCAGCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCCGAGCGCTGCGCTGCTGCTGCGAGCCACTACCGGAGGTGCT 127
Db 61 GCGCGCTCCCGCTGCCGAGCGCTGCGCTGCTGCTGCGAGCCACTACCGGAGGTGCT 120
QY 128 GCGCGTGGCAGCTTGTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGTGTGACGCGG 187
Db 121 GCGCGTGGCAGCTTGTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGTGTGACGCGG 180
QY 188 GGACCCGGGCGCTTCCGCGCGCTGTGTGCGCCAGTGTGCTGTGCTGCGCCCTGGGAGCGC 247
Db 181 GGACCCGGGCGCTTCCGCGCGCTGTGTGCGCCAGTGTGCTGTGCTGCGCCCTGGGAGCGC 240

QY	248	ACGGCCCCCCCCCCCCCTCTTCCGCCAGGTGCTCTGCTGAAGGAGCTGTGGC	307
Db	241	ACGGCCCCCCCCCCCCCTCTTCCGCCAGGTGCTCTGCTGAAGGAGCTGTGGC	300
QY	308	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGGAAGACTGTGGCTTTCGCTTCGC	367
Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGGAAGACTGTGGCTTTCGCTTCGC	360
QY	368	GCTGCTGGACGGGGCCCCGGGGGGGGCCCCCGAGGCTTCAACCAAGAGCTGGCAGCTA	427
Db	361	GCTGCTGGACGGGGCCCCGGGGGGGGCCCCCGAGGCTTCAACCAAGAGCTGGCAGCTA	420
QY	428	CCTGCCCAACACGCTGACCGACGCACTGCGGGGGAGCGGGGGCTGGGGGCTGTGCTGG	487
Db	421	CCTGCCCAACACGCTGACCGACGCACTGCGGGGGAGCGGGGGCTGGGGGCTGTGCTGG	480
QY	488	CCGCGTGGGGCGACGACGTGCTGTTCACTGCTGTGGACGCTGGCGGCTCTTTGTGCTGT	547
Db	481	CCGCGTGGGGCGACGACGTGCTGTTCACTGCTGTGGACGCTGGCGGCTCTTTGTGCTGT	540
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QY	608	TCAGGGCCCCGGCCCCCAACAGCTAGTGGACCCCGAAGCGCTGGGATGCCAAGGGC	667
Db	601	TCAGGGCCCCGGCCCCCAACAGCTAGTGGACCCCGAAGCGCTGGGATGCCAAGGGC	660
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QY	848	GCGTGGACCGAGTGACCGTGCTTCTGTGTGTGTACTGCGAGACCCGCGGAAGAC	907
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QY	908	CACCTCTTTGGAGGCGTCTCTGGCAGCGCGCACTCCACCCATCCGTGGCGCGCA	967
Db	901	CACCTCTTTGGAGGCGTCTCTGGCAGCGCGCACTCCACCCATCCGTGGCGCGCA	960
QY	968	GCACCACGCGGGCCCCCAATCCATCGCGGCCACCAAGTCCCTGGGACACGCTGTCC	1027
Db	961	GCACCACGCGGGCCCCCAATCCATCGCGGCCACCAAGTCCCTGGGACACGCTGTCC	1020
QY	1028	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGGACAAGAGGACAGCTGCG	1087
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGGACAAGAGGACAGCTGCG	1080
QY	1088	GCCCTCTTCTTACTACGCTCTGTAGGGCCAGCCTGACTGGCGCTCGGAGGCTGTGGA	1147
Db	1081	GCCCTCTTCTTACTACGCTCTGTAGGGCCAGCCTGACTGGCGCTCGGAGGCTGTGGA	1140
QY	1148	GACCATCTTCTTGGGTTCAGGCCCCCTGGATGCCAGGGACTCCCCGAGTTGCCCGCCT	1207
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RESULT 5
US-09-721-477-343
; Sequence 343, Application US/09721477
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;             Lingner, Joachim
;             Nakamura, Toru
;             Chapman, Karen B.
;             Morin, Gregg B.
;             Harley, Calvin B.
;             Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,477
; FILING DATE: 22-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
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APPLICATION NUMBER: US 08/851,843
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note="refined sequence of hprt cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 343:
US-09-721-477-343

Query Match 99.4%; Score 3982.6; DB 29; Length 4037;
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Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;

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QY 3512 CACACCCAGGCCCGCACCCTGGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCCCTG 3571
Db 3541 CACACCCAGGCCCGCACCCTGGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCCCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTAGTGTCCGGCTGAGGCCGTGAGCGAGTGTCCAGCCAAAGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTAGTGTCCGGCTGAGGCCGTGAGCGAGTGTCCAGCCAAAGGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGGCGCTCGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGGCGCTCGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTTCCCAATAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTTCCCAATAGGAATAGTCCATCC 3780

QY 2912 CGGCTTCAAGGCTGGAGGAACATGCGTCCAAACTCTTTGGGCTCTTGCGGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGAGGAACATGCGTCCAAACTCTTTGGGCTCTTGCGGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGGATTGAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3031
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QY 3092 TCAGCAAGTTTGAAGAACCACATTTTCTGCGCTCATCTCTGACACGGCTCCCT 3151
Db 3121 TCAGCAAGTTTGAAGAACCACATTTTCTGCGCTCATCTCTGACACGGCTCCCT 3180
QY 3152 CTGCTACTCCATCTCTGAAGCCAGACGAGGATGTGCTGGGGGCCCAAGGGCGCCG 3211
Db 3181 CTGCTACTCCATCTCTGAAGCCAGACGAGGATGTGCTGGGGGCCCAAGGGCGCCG 3240
QY 3212 CGGCTCTGCTCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271
Db 3241 CGGCTCTGCTCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGGTGTCACTACCTGACCTCTCTGGGGTCACTCAGACGAGCCAGACGCA 3331
Db 3301 GACTCGACACCGGTGTCACTACCTGACCTCTCTGGGGTCACTCAGACGAGCCAGACGCA 3360
QY 3332 GCTGAGTCGAAAGCTCCCGGGGAGCAGCTGACTGCCCTGAGGCGCCAGCCAAACCCGCG 3391
Db 3361 GCTGAGTCGAAAGCTCCCGGGGAGCAGCTGACTGCCCTGAGGCGCCAGCCAAACCCGCG 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCACTCTGAGTGTGAGTGGCCACCGCCCAACAGCCAGCCGA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCACTCTGAGTGTGAGTGGCCACCGCCCAACAGCCAGCCGA 3480
QY 3452 GAGCAACACACAGCAGCCCTGTCAACGCGGGGCTTACGTCCCAAGGAGAGGGCGCGCC 3511
Db 3481 GAGCAACACACAGCAGCCCTGTCAACGCGGGGCTTACGTCCCAAGGAGAGGGCGCGCC 3540
QY 3512 CACACCCAGGCGCGCAGCCGTGGAGTCTGAGGCGCTGAGTGAAGTGTGGCCGAGGCGCTG 3571
Db 3541 CACACCCAGGCGCGCAGCCGTGGAGTCTGAGGCGCTGAGTGAAGTGTGGCCGAGGCGCTG 3600
QY 3572 CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGCGCTGAGTGAAGTGTGG 3631
Db 3601 CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGCGCTGAGTGAAGTGTGG 3660
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Db 3661 GAGTGTCCAGCACACCTGCGCTTCTCACTTCCACAGGCGTGGCGCTCCACCCCA 3720
QY 3692 GGGCAGCTTTTCTCTCACAGAGCGCGGCTTCCACTCCCAATAGGAATAGTCCATCC 3751
Db 3721 GGGCAGCTTTTCTCTCACAGAGCGCGGCTTCCACTCCCAATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTCGCCATTTGTACACCCCTGCGGCTGCGCTTCTTCCACCCCCACCATCC 3811
Db 3781 CCAGATTCGCCATTTGTACACCCCTGCGGCTGCGCTTCTTCCACCCCCACCATCC 3840
QY 3812 AGGTGAGAGACCTTGAGAAAGGACCTGGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3871
Db 3841 AGGTGAGAGACCTTGAGAAAGGACCTGGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGGCGAGGACCTGACCTGATGGGGTCCCTGTGGGTCAAAATTGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCTGACCTGATGGGGTCCCTGTGGGTCAAAATTGGGG 3960
QY 3932 GAGTGCTGTGGAGTAAATATGATATATGAGTTTTCAGTTTGAAGAAAAA 3991
Db 3961 GAGTGCTGTGGAGTAAATATGATATATGAGTTTTCAGTTTGAAGAAAAA 4020
QY 3992 AAAAAAAAAAAAAA 4006

Db 4021 AAAAAAAAAAAAAA 4035

RESULT 7
US-08-974-524E-117
: Sequence 117, Application US/08974524E
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
: Lingner, Joachim
: Nakamura, Toru
: Chapman, Karen B.
: Morin, Gregg B.
: Harley, Calvin B.
: Andrews, William H.
: TITLE OF INVENTION: Telomerase Reverse Transcriptase
: NUMBER OF SEQUENCES: 477
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/974,524E
: FILING DATE: 19-Nov-1997
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/724,643
: FILING DATE: 01-Oct-1996
: APPLICATION NUMBER: US 08/844,419
: FILING DATE: 18-Apr-1997
: APPLICATION NUMBER: US 08/846,017
: FILING DATE: 25-Apr-1997
: APPLICATION NUMBER: US 08/851,843
: FILING DATE: 06-May-1997
: APPLICATION NUMBER: US 08/854,050
: FILING DATE: 09-May-1997
: APPLICATION NUMBER: US 08/911,312
: FILING DATE: 14-Aug-1997
: APPLICATION NUMBER: US 08/912,951
: FILING DATE: 14-Aug-1997
: APPLICATION NUMBER: US 08/915,503
: FILING DATE: 14-Aug-1997
: APPLICATION NUMBER: WO PCT/US97/17618
: FILING DATE: 01-Oct-1997
: APPLICATION NUMBER: WO PCT/US97/17885
: FILING DATE: 01-Oct-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Einhorn, Gregory P.
: REGISTRATION NUMBER: 38,440
: REFERENCE/DOCKET NUMBER: 015389-002950US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 117:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4038 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 56..3454
: OTHER INFORMATION: /note= "refined hTRR DNA sequence"
: SEQUENCE DESCRIPTION: SEQ ID NO: 117:

US-08-974-524E-117

Query Match	99.4%;	Score 3982.6;	DB 13;	Length 4038;
Best Local Similarity	98.9%;	Pred. No. 6.4e-140;		
Matches 3992; Conservative	4;	Mismatches 3;	Indels 36;	Gaps 1;

QY	8	GCAGCGCTGCCTCTGCTGCTGCGACAGTGGGAAGCCCTGGGCCCCGGCCACCCCGCGGATGCC	67
Db	1	GCAGCGCTGCGTCTCTGCTGCGACAGTGGGAAGCCCTGGGCCCCGGCCACCCCGCGGATGCC	60
QY	68	GCAGCGTCCCCCGCTGCGCGAGCCGTGCGCTCTCTGCTGCGACAGCCACTACCGGAGGTGCT	127
Db	61	GCAGCGTCCCCCGCTGCGCGAGCCGTGCGCTCTCTGCTGCGACAGCCACTACCGGAGGTGCT	120
QY	128	GCCGCGTGGCCACAGTTCTGTGCGCGCCCTGGGGCCCCCAGGGGCTGGCGGCTGTGTGACGCGCG	187
Db	121	GCCGCGTGGCCACAGTTCTGTGCGCGCCCTGGGGCCCCCAGGGGCTGGCGGCTGTGTGACGCGCG	180
QY	188	GGACCGGGGCGGCTTTCGGCGCCCTGTGGGCCAGTGGCTGTGTGTGCTGCTGCGGAGCGC	247
Db	181	GGACCGGGGCGGCTTTCGGCGCCCTGTGGGCCAGTGGCTGTGTGTGCTGCTGCGGAGCGC	240
QY	248	ACGCGCGCCCCCGCGCCCGCTCTTCGCGCAGGTGTCTGCTGCTGAAGAGCTGTGTGC	307
Db	241	ACGCGCGCCCCCGCGCCCGCTCTTCGCGCAGGTGTCTGCTGCTGAAGAGCTGTGTGC	300
QY	308	CCGAGTGTCTGCAGAGGCTGTGTGCGAGCGCGCGCGGAAGACGTGTGTGCTTCGCGCTTCGC	367
Db	301	CCGAGTGTCTGCAGAGGCTGTGTGCGAGCGCGCGCGGAAGACGTGTGTGCTTCGCGCTTCGC	360
QY	368	GCTGTGTGAGCGGGGCGCGCGGGGGCCCCCGCGAGGCGCTTCACACACAGCGTGGCGACGTA	427
Db	361	GCTGTGTGAGCGGGGCGCGCGGGGGCCCCCGCGAGGCGCTTCACACACAGCGTGGCGACGTA	420
QY	428	CTTGCCCAACACGGGTGACCGAGCGCACTGCGGGGGAGCGGGGCGTGGGGGCTGTCTGTCG	487
Db	421	CTTGCCCAACACGGGTGACCGAGCGCACTGCGGGGGAGCGGGGCGTGGGGGCTGTCTGTCG	480
QY	488	CCGCGTGGGGCGACGACGTGTGTGTTACCTGTCTGGCACGCTGGCGGCTTTGTGTCTGT	547
Db	481	CCGCGTGGGGCGACGACGTGTGTGTTACCTGTCTGGCACGCTGGCGGCTTTGTGTCTGT	540
QY	548	GCGTCCCAAGCTGCGCTTACACAGTGTGCGGGCGCGCGCTGTACCACTCGCGCTGCGCAC	607
Db	541	GCGTCCCAAGCTGCGCTTACACAGTGTGCGGGCGCGCGCTGTACCACTCGCGCTGCGCAC	600
QY	608	TCAGGCGCGGGGCGCCCGCCACACAGCTAGTGGACCCCCGAAGGCGTGTGGGATGCCAAGGGG	667
Db	601	TCAGGCGCGGGGCGCCCGCCACACAGCTAGTGGACCCCCGAAGGCGTGTGGGATGCCAAGGGG	660
QY	668	CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCCCCTGGGCTTGCCAGCCCCGGGTGCGAG	727
Db	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCCCCTGGGCTTGCCAGCCCCGGGTGCGAG	720
QY	728	GAGGCGCGGGGCGCACTGCCAGCCGAAGTCTGCCGTTGGCCCCAAGAGGCCAGGCGTGGCGC	787
Db	721	GAGGCGCGGGGCGCACTGCCAGCCGAAGTCTGCCGTTGGCCCCAAGAGGCCAGGCGTGGCGC	780
QY	788	TGCCCCGTGAGCCGGAAGCGGAGCGCCGTTGGGACAGGGGTCTGGGCCACCCGGGACGAGC	847
Db	781	TGCCCCGTGAGCCGGAAGCGGAGCGCCGTTGGGACAGGGGTCTGGGCCACCCGGGACGAGC	840
QY	848	GCGTGAACCGAGTGAACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	907
Db	841	GCGTGAACCGAGTGAACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
QY	908	CACCTTTTGGAGGTTGGGCTCTCTGTGCACGCGGCCACTTCCACCCTCCGTGGGCGCGCA	967
Db	901	CACCTTTTGGAGGTTGGGCTCTCTGTGCACGCGGCCACTTCCACCCTCCGTGGGCGCGCA	960
QY	968	GCACCAAGCGGGCGCCCATCAATCGCGGACCAACAGTCCCTGGGACACGCGCTTGTCTC	1027
Db	961	GCACCAAGCGGGCGCCCATCAATCGCGGACCAACAGTCCCTGGGACACGCGCTTGTCTC	1020

QY	1028	CCCGGTGTACGCCGAGAGACCAAGCACTTCTCTTACTCTCAGGGCAGCAAGAGGACAGCTGGC	1087
Db	1021	CCCCGTTGTACGCCGAGAGACCAAGCACTTCTCTTACTCTCAGGGCAGCAAGAGGACAGCTGGC	1080
QY	1088	GGCCTCTCTTCTACTACTCAGCTCTCTGAGGGCCAGCCGACTGGCGCTCGGAGGCTCGTGG	1147
Db	1081	GGCCTCTCTTCTACTACTCAGCTCTCTGAGGGCCAGCCGACTGGCGCTCGGAGGCTCGTGG	1140
QY	1148	GACCATCTTTCTGEGGTTCCAGGCCCCGTGATGCCAGGACTCCCCCGCAGGTTGCCCGCCT	1207
Db	1141	GACCATCTTTCTGEGGTTCCAGGCCCCGTGATGCCAGGACTCCCCCGCAGGTTGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGGCCCTGTTCTGAGACTGCTTTGGGAACCAACCGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGGCCCTGTTCTGAGACTGCTTTGGGAACCAACCGCGCA	1260
QY	1268	GTGCCCCCTACGGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACACCCAGC	1327
Db	1261	GTGCCCCCTACGGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACACCCAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCAAGGCTCTGTGGCGGGCCCCCGAGAGAGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCAAGGCTCTGTGGCGGGCCCCCGAGAGAGGA	1380
QY	1388	CACAGACCCCGCTGCGCTGGTGCAGCTGCTCCGCCAGACAGCAGCCCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCGCTGCGCTGGTGCAGCTGCTCCGCCAGACAGCAGCCCCCTGGCAGGTGA	1440
QY	1448	CGGCTTCGTGCGGGCCCTGCTCGCCCGCGCTGTGACCCCAAGGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGGCCCTGCTCGCCCGCGCTGTGACCCCAAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGCCGTTCTCAGGAACACCAAGAATTCTCTCCCTGGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGCCGTTCTCAGGAACACCAAGAATTCTCTCCCTGGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGACTGGCTTGCTGCGCAG	1627
Db	1561	GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGACTGGCTTGCTGCGCAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTTCGGCCGAGAGCACCCTCTGCGTGAAGAGATCCTGGC	1687
Db	1621	GAGCCCAAGGGGTGGCTGTGTTCGGCCGAGAGCACCCTCTGCGTGAAGAGATCCTGGC	1680
QY	1688	CAAGTTCTCTGCACTGGGCTGATGAGTGTGTACGTGCTGCAAGCTGCTCAGGCTCTTCTTTA	1747
Db	1681	CAAGTTCTCTGCACTGGGCTGATGAGTGTGTACGTGCTGCAAGCTGCTCAGGCTCTTCTTTA	1740
QY	1748	TGTCAACGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTTACCCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCAACGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTTACCCGGAAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC	1867
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCTGCTGACTGCACAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCTGCTGACTGCACAGACTCCG	1920
QY	1928	CTTTCATCCCCCAAGCCTGACGGGGCTGCGGGCGATTGTGAACATGACTACGTCGFGGGAGC	1987
Db	1921	CTTTCATCCCCCAAGCCTGACGGGGCTGCGGGCGATTGTGAACATGACTACGTCGFGGGAGC	1980
QY	1988	CAGAAGCTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACCTGTT	2047
Db	1981	CAGAAGCTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACCTGTT	2040
QY	2048	CAGCGTCTCAACTACGAGCGGGGCGGGGCGCCCGGCTCTGCGGGCCTCTGTGCTGGG	2107
Db	2041	CAGCGTCTCAACTACGAGCGGGGCGGGGCGCCCGGCTCTGCGGGCCTCTGTGCTGGG	2100

QY 2108 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTCGGGCCAGGACCC 2167
Db 2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTCGGGCCAGGACCC 2160
QY 2168 GCGGCGTGAAGTGTACTTTGTCAGAGGTGATGTAGCGGGCGGTACGACACCATCCCA 2191
Db 2161 GCGGCGTGAAGTGTACTTTGTCAGAGGTGATGTAGCGGGCGGTACGACACCATCCCA 2220
QY 2192 GGACAGGCTCAGGAGGTGATCGCCAGCATCATCAACCCAGAAACGTAAGTGCCTGCG 2251
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QY 2252 TCGGTATGCGGTGTCAGAGGCGCCCATGGCGACGTCGCGCAAGGCTTCAAGAGCCA 2311
Db 2281 TCGGTATGCGGTGTCAGAGGCGCCCATGGCGACGTCGCGCAAGGCTTCAAGAGCCA 2340
QY 2312 CGTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGCTCAGCTGAGGA 2371
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QY 2432 CAGTGGCTCTTGCAGCTCTCTACGCTTCATGTGCCACACGCGCGTGCATCAGGGG 2491
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Db 2581 CAGCCTGCTACGCGCGACATGAGAAACAGCTGTTGCGGGGATCGCGGGAGCGGCT 2640
QY 2612 GCTCCTGCTTGTGGATGATTTCTGTTGGTGACACCTCACCTCACCCAGCGAAAC 2671
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QY 2672 CTTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGGTGAACCTGCGGAA 2731
Db 2701 CTTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGGTGAACCTGCGGAA 2760
QY 2732 GACAGTGGTGAACCTCCCTGTAGAAAGCAGGCGCTGGGTGCGAGCGCTTGTTCAGAT 2791
Db 2761 GACAGTGGTGAACCTCCCTGTAGAAAGCAGGCGCTGGGTGCGAGCGCTTGTTCAGAT 2820
QY 2792 GCGGCGCAGCGGCTATTCCTGCTGCGGCGCTGCTGCTGATACCCGAGCCCTGAGGT 2851
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QY 3032 CAAGATCCTCTGCTGAGGCGTACAGGTTTTCAGCGCATGTGCTGAGCTCCCATTTCA 3091
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QY 3092 TCAGCAAGTTTGAAGAACCCACATTTTCTCGCGCTCATCTGACAGGCGCTCCCT 3151
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QY 3152 CTGCTACTCCATCTTGAAAGCCAGAACGACGAGGATGTCGCTGGGGGCCAAGGGCGCGC 3211

Db 3181 CTGCTACTCCATCTGAAAGCCAGAAAGCAGGAGATGTCGCTGGGGGCCAAGGGCGCGC 3240
QY 3212 CGGCCCTGCCCCCTCCGAGGGCGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAGCT 3271
Db 3241 CGGCCCTGCCCCCTCCGAGGGCGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAGCT 3300
QY 3272 GACTGCACACCGTGTACCTACGTGCGACCTCTGGGGTCACTCAGAGCAGCCAGACGCA 3331
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QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGAGTGTATGGCCACCCGCCACAGCCAGCCGA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGTGTATGGCCACCCGCCACAGCCAGCCGA 3480
QY 3452 GAGCAGACACGACGACCCCTGTACAGCGCGGCTCTACGTCCAGGAGGAGGGCGGCGC 3511
Db 3481 GAGCAGACACGACGACCCCTGTACAGCGCGGCTCTACGTCCAGGAGGAGGGCGGCGC 3540
QY 3512 CACACCCAGGCGCGCACCCGCTGGAGTCTGAGGCGCTGAGTGTATTTGGCCGAGGCGCTG 3571
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QY 3572 CATGTCCGCTGAAGGCTGAGTGTCCGCGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGCGCT 3631
Db 3601 CATGTCCGCTGAAGGCTGAGTGTCCGCGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGCGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGGCTTCACTTCCACAGAGGCTGGCGCTGCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGGCTTCACTTCCACAGAGGCTGGCGCTGCCACCCCA 3720
QY 3692 GGGCAGCTTTCTCACCAGAGGCGCGCTTCCACTCCCAACATAGTAAGTAAGTCCATCC 3751
Db 3721 GGGCAGCTTTCTCACCAGAGGCGCGCTTCCACTCCCAACATAGTAAGTCCATCC 3780
QY 3752 CCAGATTCGCCATGTTTACCCCTGCGCCCTGCCCTCTTGGCTTCCACCCCAACATCC 3811
Db 3781 CCAGATTCGCCATGTTTACCCCTGCGCCCTGCCCTCTTGGCTTCCACCCCAACATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3871
Db 3841 AGGTGAGACCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG 3900
QY 3872 CCCTGTACAGGCGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGGG 3931
Db 3901 CCCTGTACAGGCGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGGG 3960
QY 3932 GAGGTGCTGGGAGTAAATACTGATATATGAGTTTTCAGTTTGAAGGAGGAGGAGGAGG 3991
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QY 3992 AAAAAAAAAAAAAA 4006
Db 4021 AAAAAAAAAAAAAA 4035

RESULT 8
US-08-974-584C-117
Sequence 117, Application US/08974584C

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 479

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,584C
FILING DATE: 19-Nov-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elmhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-0029500S
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 4038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined hTERT DNA sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-08-974-584C-117
Query Match 99.4%; Score 3982.6; DB 13; Length 4038;
Best Local Similarity 98.9%; Pred. No. 6.4e-140;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCTCTGCTGCGACAGTGGGAAGCCCTGGCCCCCGGCGATGCC 67
DB 1 GCAGCGCTGCTCTGCTGCGACAGTGGGAAGCCCTGGCCCCCGGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGAGCGCTGCTGCTGCGAGCCACTACCGGAGGTGCT 127
DB 61 GCGCGCTCCCGCTGCGAGCGCTGCTGCTGCTGCGAGCCACTACCGGAGGTGCT 120
QY 128 GCGCGTGGCCAGTTCGTGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 187
DB 121 GCGCGTGGCCAGTTCGTGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180

QY 188 GGACCCGGCGGCTTTCCGCGCGCTGTGGCCAGTGCCCTGTGTGCGTGCCTGGAGCGC 247
DB 181 GGACCCGGCGGCTTTCCGCGCGCTGTGGCCAGTGCCCTGTGTGCGTGCCTGGAGCGC 240
QY 248 ACGGCG 307
DB 241 ACGGCG 300
QY 308 CCGAGTCTGCAGAGGCTGTGGAGAGCGCGCGCGGCGGAAGACGTGTGCGCTTGGCTGCG 367
DB 301 CCGAGTCTGCAGAGGCTGTGGAGAGCGCGCGCGGCGGAAGACGTGTGCGCTTGGCTGCG 360
QY 368 GCTGCTGGACGGGGCGCGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 427
DB 361 GCTGCTGGACGGGGCGCGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 420
QY 428 CCGCCCAACAGGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGTGCTGCG 487
DB 421 CCGCCCAACAGGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGTGCTGCG 480
QY 488 CCGCGTGGCGGACGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
DB 481 CCGCGTGGCGGACGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GCGTCCCGAGCTGCGCGCTTACCAAGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCG 607
DB 541 GCGTCCCGAGCTGCGCGCTTACCAAGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCG 600
QY 608 TCAGCG 667
DB 601 TCAGCG 660
QY 668 CTGAACCATAGCGTACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
DB 661 CTGAACCATAGCGTACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGCGCGCGGGGAGTGCAGCGCGAAGTCTGCGCGTGTGCGCAAGAGGCGCGAGCGCG 787
DB 721 GAGCGCGCGGGGAGTGCAGCGCGAAGTCTGCGCGTGTGCGCAAGAGGCGCGAGCGCG 780
QY 788 TGCCCGTGAAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
DB 781 TGCCCGTGAAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 848 GCGTGGACCGAGTGAACCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 907
DB 841 GCGTGGACCGAGTGAACCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 900
QY 908 CACCTCTTTGAGGGGTGCGCTCTGTGCGACGCGCGCACCTCCACCCATCCGTGGCGCGCA 967
DB 901 CACCTCTTTGAGGGGTGCGCTCTGTGCGACGCGCGCACCTCCACCCATCCGTGGCGCGCA 960
QY 968 GCACACGCGGGCGTCC 1027
DB 961 GCACACGCGGGCGTCC 1020
QY 1028 CCGGCTGTACGCGCGGAGACCAAGCACTTCTCTACTCTCTAGGGGAGCAAGAGAGAGCTGCG 1087
DB 1021 CCGGCTGTACGCGCGGAGACCAAGCACTTCTCTACTCTCTAGGGGAGCAAGAGAGAGCTGCG 1080
QY 1088 GCGCTCCCTCTCTACTAGCTCTCTGAGGGCGCAAGCGCTGACTGGCGGTGGAGGCTGTGA 1147
DB 1081 GCGCTCCCTCTCTACTAGCTCTCTGAGGGCGCAAGCGCTGACTGGCGGTGGAGGCTGTGA 1140
QY 1148 GACCATCTTTCTGGGTTCCAGGCGCGCTGATGCCAGGAGCTCCCGGAGGTTGCCCGCGCT 1207
DB 1141 GACCATCTTTCTGGGTTCCAGGCGCGCTGATGCCAGGAGCTCCCGGAGGTTGCCCGCGCT 1200
QY 1208 GCGCCAGCGCTACTGGCAATGGCGCGCGCGCTTCTGTGAGCTGCTTGGGAACACCGCGCA 1267
DB 1201 GCGCCAGCGCTACTGGCAATGGCGCGCGCGCTTCTGTGAGCTGCTTGGGAACACCGCGCA 1260

QY 1268 GTGCCCCCTACGGGGTGTCTCCTCAAGACCGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGC 1327
Db 1261 GTGCCCCCTACGGGGTGTCTCCTCAAGACCGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGC 1320
QY 1328 AGCCGGTGTCTGTGCCCCGGAGAAAGCCCGAGGGCTGTGTGGCGCCCCCGAGGAGGAGGA 1387
Db 1321 AGCCGGTGTCTGTGCCCCGGAGAAAGCCCGAGGGCTGTGTGGCGCCCCCGAGGAGGAGGA 1380
QY 1388 CACAGACCCCCGCTGCTGTGTGAGCTGTCTCCGACAGACAGAGCCCTGTGAGGTGA 1447
Db 1381 CACAGACCCCCGCTGCTGTGTGAGCTGTCTCCGACAGACAGAGCCCTGTGAGGTGA 1440
QY 1448 CGGCTTGTGTGGGCTGCTGCTGCGCGGCTGTGTGCCCCAGGCTCTGGGGCTCCAGGCA 1507
Db 1441 CGGCTTGTGTGGGCTGCTGCTGCGCGGCTGTGTGCCCCAGGCTCTGGGGCTCCAGGCA 1500
QY 1508 CAACGAACGCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1567
Db 1501 CAACGAACGCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGTTGGCTGCGCAG 1627
Db 1561 GCTCTGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGTTGGCTGCGCAG 1620
QY 1628 GAGCCCAAGGGTGGCTGTGTCCGCGCAGACACCGCTGTGCTGAGAGATCCTGGC 1687
Db 1621 GAGCCCAAGGGTGGCTGTGTCCGCGCAGACACCGCTGTGCTGAGAGATCCTGGC 1680
QY 1688 CAAGTTCCTGCACTGGCTGATGATGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTA 1747
Db 1681 CAAGTTCCTGCACTGGCTGATGATGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTA 1740
QY 1748 TGTACGAGAGACCAAGCTTTCAAAGAAGAGGCTTTTCTACCGGAAGAGTGTCTGGAG 1807
Db 1741 TGTACGAGAGACCAAGCTTTCAAAGAAGAGGCTTTTCTACCGGAAGAGTGTCTGGAG 1800
QY 1808 CAAGTTCGAAGCATTTGGAATCAGACAGACTTTGAAGAAGGGTGACGTGCGGAGAGCTGTC 1867
Db 1801 CAAGTTCGAAGCATTTGGAATCAGACAGACTTTGAAGAAGGGTGACGTGCGGAGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAGGCGACATCGGGAAGCCAGGCCCCCTGCTGACGTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTCAGGCGACATCGGGAAGCCAGGCCCCCTGCTGACGTCCAGACTCCG 1920
QY 1928 CTTCAATCCCAAGCTGACGGGCTGCGCGATTTGAACATGAGCTGCTGGGAGC 1987
Db 1921 CTTCAATCCCAAGCTGACGGGCTGCGCGATTTGAACATGAGCTGCTGGGAGC 1980
QY 1988 CAGAAGCTCCGACAGAAAGAGGGCGGCTGCTACCTCGAGGCTGAAGGCACTGTT 2047
Db 1981 CAGAAGCTCCGACAGAAAGAGGGCGGCTGCTACCTCGAGGCTGAAGGCACTGTT 2040
QY 2048 CAGCGTGTCAACTACGAGCGGGCGGCGCCCCGCTCCTGGGCGCTCTGTGTTGG 2107
Db 2041 CAGCGTGTCAACTACGAGCGGGCGGCGCCCCGCTCCTGGGCGCTCTGTGTTGG 2100
QY 2108 CCTGAGCATATCCACAGGGGCTGGCGACTTCTGTGCTGTGCTGTGCGGCCCCAGGAGCC 2167
Db 2101 CCTGAGCATATCCACAGGGGCTGGCGACTTCTGTGCTGTGCTGTGCGGCCCCAGGAGCC 2160
QY 2168 GCGGCTGTGACTGTA-----CATCCCCCA 2191
Db 2161 GCGGCTGTGACTGTA-----CATCCCCCA 2220
QY 2192 GGACAGGCTTCAGGAGGTATCGCCAGCATATCAAAACCCAGAAACAGTACTGCTGG 2251
Db 2221 GGACAGGCTTCAGGAGGTATCGCCAGCATATCAAAACCCAGAAACAGTACTGCTGG 2280
QY 2252 TCGGTATGCGGTGTCAGAAAGCGCGCATGGGACGTCCGCAAGGCTTCAAGAGCCA 2311
Db 2281 TCGGTATGCGGTGTCAGAAAGCGCGCATGGGACGTCCGCAAGGCTTCAAGAGCCA 2340
QY 2312 CGTCTTACTTGAAGACCTCAGCGCGTACATGCGAGACAGTTCGTGCTCACCTGACAGA 2371

Db 2341 CGTCTTACTTGAAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400
QY 2372 GACCAGCCCGCTGAGGGATGCCGTGCTCATGACAGACAGAGCTCCTCCCTGAATGAGGCCAG 2431
Db 2401 GACCAGCCCGCTGAGGGATGCCGTGCTCATGACAGACAGAGCTCCTCCCTGAATGAGGCCAG 2460
QY 2432 CAGTGGCTCTTCGACGCTTCTCTACGCTTCATGTGCCACCACGCGCGTGCATCAGGGG 2491
Db 2461 CAGTGGCTCTTCGACGCTTCTCTACGCTTCATGTGCCACCACGCGCGTGCATCAGGGG 2520
QY 2492 CAAGTCTACGTCCAGTGCAGAGGGATCCCGAGGGCTCCATCCTCTCCAGCGCTGCTG 2551
Db 2521 CAAGTCTACGTCCAGTGCAGAGGGATCCCGAGGGCTCCATCCTCTCCAGCGCTGCTG 2580
QY 2552 CAGCCTGTGCTACGCGCAGACATGAGAAACAGCTGTTGCGGGGATTCGGCGGAGCGGCT 2611
Db 2581 CAGCCTGTGCTACGCGCAGACATGAGAAACAGCTGTTGCGGGGATTCGGCGGAGCGGCT 2640
QY 2612 GCTCCTGCGTTGGTGGATGATTTCTGTGGTGAACACTCACCTCACCCACGCGAAAC 2671
Db 2641 GCTCCTGCGTTGGTGGATGATTTCTGTGGTGAACACTCACCTCACCCACGCGAAAC 2700
QY 2672 CTTCTCAGAGACCTGTGTCGAGGTGTCCCTGAGTATGGCTGCGGTGAACCTTGGGAA 2731
Db 2701 CTTCTCAGAGACCTGTGTCGAGGTGTCCCTGAGTATGGCTGCGGTGAACCTTGGGAA 2760
QY 2732 GACAGTGTGAACCTCCCTGTAGAAGACGAGCCCTGGGTGGACGCGCTTTGTTAGAT 2791
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QY 2792 GCGGCGCACGCGCTATTTCCCTGTGCGCGCTGCTGCTGATACCGGAGCCCTGGAGGT 2851
Db 2821 GCGGCGCACGCGCTATTTCCCTGTGCGCGCTGCTGCTGATACCGGAGCCCTGGAGGT 2880
QY 2852 GCAGAGGACTTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGCTCACCTTCAACCG 2911
Db 2881 GCAGAGGACTTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGCTCACCTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGTCTTGGGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGTCTTGGGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGGATTTCGAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA 3031
Db 3001 TCACAGCCTGTTTCTGGATTTCGAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA 3060
QY 3032 CAAGATCCTCTGCTGACAGGCGTACAGGTTTCAACGATGTGTGCTGAGCTCCCATTTCA 3091
Db 3061 CAAGATCCTCTGCTGACAGGCGTACAGGTTTCAACGATGTGTGCTGAGCTCCCATTTCA 3120
QY 3092 TCAGCAAGTTTGAAGAAGCCACATTTTCTGCGCGTCAITCTGACAGCGGCTCCCT 3151
Db 3121 TCAGCAAGTTTGAAGAAGCCACATTTTCTGCGCGTCAITCTGACAGCGGCTCCCT 3180
QY 3152 CTGCTACTCCATCTGAAAAGCCAAAGAACGAGGATGTGCTGGGGCCAAAGGCGCGC 3211
Db 3181 CTGCTACTCCATCTGAAAAGCCAAAGAACGAGGATGTGCTGGGGCCAAAGGCGCGC 3240
QY 3212 CGGCGCTGTGCGCTCCGAGGCGGTGACGTGGCTGTGCCACCAAGCAATTCTGCTCAAGCT 3271
Db 3241 CGGCGCTGTGCGCTCCGAGGCGGTGACGTGGCTGTGCCACCAAGCAATTCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGTGTACACTACGTGCGCACTCTGGGGTCACTCAGACAGCCAGACGCA 3331
Db 3301 GACTCGACACCGTGTACACTACGTGCGCACTCTGGGGTCACTCAGACAGCCAGACGCA 3360
QY 3332 GCTGAGTGGGAAGCTCCCGGGAGCAGCGTGAAGTCCCTGGAGGGCCGCAAGCCAGCCG 3391
Db 3361 GCTGAGTGGGAAGCTCCCGGGAGCAGCGTGAAGTCCCTGGAGGGCCGCAAGCCAGCCG 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGAGCTGATGGCCACCCGCGCACAGCCAGGCGCA 3451

Db 3421 ACTGCCCTCAGACTTTCAGACCAACCATTCCTGACTGATGCGCACCCGCCACACAGCCAGGCGCA 3480
QY 3452 GAGCAGACACAGCAGACCCCTGTTCAGCGCCGGGCTCTACGTCCAGGAGGAGGGCGGCC 3511
Db 3481 GAGCAGACACAGCAGACCCCTGTTCAGCGCCGGGCTCTACGTCCAGGAGGAGGGCGGCC 3540
QY 3512 CACACCCAGGCGCCGCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCTG 3571
Db 3541 CACACCCAGGCGCCGCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCTG 3600
QY 3572 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGTCACAGGCT 3631
Db 3601 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGTCACAGGCT 3660
QY 3632 GAGTGTCCAGCAGACCTGCGCTCTTCACTTCCACACAGGCTGGCGCTCGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGCAGACCTGCGCTCTTCACTTCCACACAGGCTGGCGCTCGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCCATCCACAGAGCGCGGCTTCCACTCCACATAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTTCTCACCAGAGCGCGGCTTCCACTCCACATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTCGCATTTGTTACCCCTGCGCTGCGCTTCTTCCCTTCCACCCCAACCATCC 3811
Db 3781 CCAGATTCGCATTTGTTACCCCTGCGCTGCGCTTCTTCCCTTCCACCCCAACCATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAAGACCTGGGAGCTGTGGGAATTTGAGTGAACAAAGTGTG 3871
Db 3841 AGGTGAGACCCCTGAGAAAGACCTGGGAGCTGTGGGAATTTGAGTGAACAAAGTGTG 3900
QY 3872 CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGCTCCTGTGGTCAAAATTTGGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGCTCCTGTGGTCAAAATTTGGGGG 3960
QY 3932 GAGTGTGTGGGAGTAATACTGATATATATAGTTTTTCAGTTTGAIAAAAAAAAA 3991
Db 3961 GAGTGTGTGGGAGTAATACTGATATATATAGTTTTTCAGTTTGAIAAAAAAAAA 4020
QY 3992 AAAAAAAAAAAAAA 4006
Db 4021 AAAAAAAAAAAAAA 4035

RESULT 9
US-09-026-981-35
: Sequence 35, Application US/09026981
: GENERAL INFORMATION:
: APPLICANT: Counter, Christopher M.
: APPLICANT: Meyerson, Matthew
: APPLICANT: Weinberg, Robert A.
: TITLE OF INVENTION: Telomerase Catalytic Subunit Gene and
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Milltia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/026,981
: FILING DATE: 20-FEB-1998.
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/064,322
: FILING DATE: 30-OCT-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/055,762

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,549
; FILING DATE: 01-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,151
; FILING DATE: 20-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/038,750
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH197-11p4AM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-026-981-35

Query Match 99.2%; Score 3973.8; DB 14; Length 4023;
Best Local Similarity 99.1%; Pred. No. 1.4e-139;
Matches 3985; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

QY 5 CAGGACGCGCTGCTGCTGCGCAGCTGGGAGAGCCCTGCGCCCGCCACCCCGCGAT 64
Db 1 CAGGACGCGCTGCTGCTGCGCAGCTGGGAGAGCCCTGCGCCCGCCACCCCGCGAT 60
QY 65 GCGCGCGCTCCCGCGCTGCGGAGCCGCTGCTGCTGCTGCGCAGCCACTACCGGAGGT 124
Db 61 GCGCGCGCTCCCGCGCTGCGGAGCCGCTGCTGCTGCTGCGCAGCCACTACCGGAGGT 120
QY 125 GCTGCGCTGGCAGCTTCTGCGCGCGCGCTGGGGCCCGCAGGCGCTGGTGCAGCG 184
Db 121 GCTGCGCTGGCAGCTTCTGCGCGCGCGCTGGGGCCCGCAGGCGCTGGTGCAGCG 180
QY 185 CCGGAGCCCGGCGCTTCCCGCGCGCTGCTGCGCCAGTGCCTGTGCTGCGCTGGGA 244
Db 181 CCGGAGCCCGGCGCTTCCCGCGCGCTGCTGCGCCAGTGCCTGTGCTGCGCTGGGA 240
QY 245 CGCAGCGCGCGCGCGCGCGCGCGCTTCCCGCAGGTGCTGCTGCTGAGGAGCTGT 304
Db 241 CGCAGCGCGCGCGCGCGCGCGCGCTTCCCGCAGGTGCTGCTGCTGAGGAGCTGT 300
QY 305 GCGCCGAGTGTGTCAGAGCTGTGCGAGCGCGCGCGCGGAGAGAGCTGTGCGGCTT 364
Db 301 GCGCCGAGTGTGTCAGAGCTGTGCGAGCGCGCGCGCGGAGAGAGCTGTGCGGCTT 360
QY 365 CCGGCTGCTGAGCGGGCGCGCGGGGGCGCGCGCGAGGCTTACACACAGCGTGGCAG 424
Db 361 CCGGCTGCTGAGCGGGCGCGCGGGGGCGCGCGCGAGGCTTACACACAGCGTGGCAG 420
QY 425 CTACCTGCCCAACAGGTGACCGAGCGACTGCGGGGAGCGGGGCGGTGGGGGCTGT 484
Db 421 CTACCTGCCCAACAGGTGACCGAGCGACTGCGGGGAGCGGGGCGGTGGGGGCTGT 480
QY 485 GCGCGCGGTGGGAGAGAGCTGTGTTCACTGCTGCGCACGCTGGCGCTTGTGTGCT 544
Db 481 GCGCGCGGTGGGAGAGAGCTGTGTTCACTGCTGCGCACGCTGGCGCTTGTGTGCT 540
QY 545 GGTGCTCCAGAGCTGCGCTTACAGAGGTGTGCGGGCGCGCTGTACAGCTGGCGCTGC 604
Db 541 GGTGCTCCAGAGCTGCGCTTACAGAGGTGTGCGGGCGCGCTGTACAGCTGGCGCTGC 600
QY 605 CACTCAGGCGCGCGCGCGCACAGCTAGTGAGCCCGGAGAGCGTGTGGATGCGAAGC 664
Db 601 CACTCAGGCGCGCGCGCGCACAGCTAGTGAGCCCGGAGAGCGTGTGGATGCGAAGC 660

QY	665	GGCCTGGAACCATAGCGCTCAGGAGAGGCCGGGGGTCCCCCTGGGCTCCAGCCCCGGGTGC	724
Db	661	GGCTGGAAACCATAGCGCTCAGGAGAGGCCGGGGGTCCCCCTGGGCTCCAGCCCCGGGTGC	720
QY	725	GAGAGAGCGCGGGGGCAGTGTCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGCGGTGC	784
Db	721	GAGGAGCGCGCGGGGCAgTGTCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGCGGTGC	780
QY	785	CGCTGCCCCCTGAGCCGAGAGCGGCCGCTTGGCAGGGGTCTGGGCCACCCGGGCAG	844
Db	781	CGTGTCCCCCTGAGCCGAGAGCGGCCGCTTGGGCAAGGGGTCTGGGCCACCCGGGCAG	840
QY	845	GACCGGTGAGACCGAGTGAACCGTGTCTGTGTGTGTACCTGCCAGACCCGCCGAAGA	904
Db	841	GACCGGTGAGACCGAGTGAACCGTGTCTGTGTGTGTACCTGCCAGACCCGCCGAAGA	900
QY	905	AGCCACCTCTTTGGAGGGGTGGCTCTCTGGCACGGGCCACTCCACCATCCGTGGGCCG	964
Db	901	AGCCACCTCTTTGGAGGGGTGGCTCTCTGGCACGGGCCACTCCACCATCCGTGGGCCG	960
QY	965	CCAGCACCAACGCGGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGCTTG	1024
Db	961	CCAGCACCAACGCGGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGCTTG	1020
QY	1025	TCCCCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGCAGCT	1084
Db	1021	TCCCCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGCAGCT	1080
QY	1085	GCGGCCCCCTCCTCTCTACTCAAGCTCTCTGAGGCCCAAGCCTGAGCTGGCGCTCGAGGCTGT	1144
Db	1081	GCGGCCCCCTCCTCTCTACTCAAGCTCTCTGAGGCCCAAGCCTGAGCTGGCGCTCGAGGCTGT	1140
QY	1145	GGAGACCATCTTCTGCGGTCCAGGCCCCCTGGATGCCAGGACTCCCCGCAAGTTGCCCG	1204
Db	1141	GGAGACCATCTTCTGCGGTCCAGGCCCCCTGGATGCCAGGACTCCCCGCAAGTTGCCCG	1200
QY	1205	CCTGCCCCCAGCGCTACTGGCAAAATGCGGGCCCTGTTTCTGGAAGCTGCTTGGGAACCAAGC	1264
Db	1201	CCTGCCCCCAGCGCTACTGGCAAAATGCGGGCCCTGTTTCTGGAAGCTGCTTGGGAACCAAGC	1260
QY	1265	GCAGTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCC	1324
Db	1261	GCAGTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCC	1320
QY	1325	AGCAGCCGGTGTCTGTGCCCGGGAAGAGCCCCCAGGCGTGTGGCGGGCCCCCAGAGAGA	1384
Db	1321	AGCAGCCGGTGTCTGTGCCCGGGAAGAGCCCCCAGGCGTGTGGCGGGCCCCCAGAGAGA	1380
QY	1385	GGACACAGACCCCCCGTGCCTGTGTCAGCTGTCTCCGCCAGCACAGCAGCCCCCTGGCAGGT	1444
Db	1381	GGACACAGACCCCCCGTGCCTGTGTCAGCTGTCTCCGCCAGCACAGCAGCCCCCTGGCAGGT	1440
QY	1445	GTACGGCTTGTGCGGGGCTGCCTGCGCGCGGCTGTGCCCCCAGGCTCTGGGGCTCCAG	1504
Db	1441	GTACGGCTTGTGCGGGGCTGCCTGCGCGCGGCTGTGCCCCCAGGCTCTGGGGCTCCAG	1500
QY	1505	GCACAAACGAACGCGCGCTTCTCAGGAACACCAAGAAGTTATCTCCCTGGGGGAAGCATGC	1564
Db	1501	GCACAAACGAACGCGCGCTTCTCAGGAACACCAAGAAGTTATCTCCCTGGGGGAAGCATGC	1560
QY	1565	CAAGCTCTCGCTGCAGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGC	1624
Db	1561	CAAGCTCTCGCTGCAGAGCTGACGTGGAAGATGAGCGTGCGGGCTGCGCTTGGCTGC	1620
QY	1625	CAGGAGCCCAAGGGGTGGCTGTGTTCGCGCCGACAGACACCGTCTGCGTGAGGAGATCCT	1684
Db	1621	CAGGAGCCCAAGGGGTGGCTGTGTTCGCGCCGACAGACACCGTCTGCGTGAGGAGATCCT	1680
QY	1685	GGCCCAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCCTTCTT	1744
Db	1681	GGCCCAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCCTTCTT	1740
QY	1745	TTATGTACAGGAGACCAAGCTTTCAAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTG	1804

D	b	1741	TTATGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTG	1800
Q	y	1805	GAGCAAGTTGCCAAAGCATTTGGAATCAGACAGCATTGAAGAGGGTGCAGCTGCGGGAGCT	1864
D	b	1801	GAGCAAGTTGCCAAAGCATTTGGAATCAGACAGCATTGAAGAGGGTGCAGCTGCGGGAGCT	1860
Q	y	1865	GTCGGAAGCAGAGGTTCAGGACGATCGGGAAAGCCAGGCCCCCTGCTGACGTCACAGCT	1924
D	b	1861	GTCGGAAGCAGAGGTTCAGGACGATCGGGAAAGCCAGGCCCCCTGCTGACGTCACAGCT	1920
Q	y	1925	CCGCTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTTGAAACATGGACTACGTCGTGGG	1984
D	b	1921	CCGCTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTTGAAACATGGACTACGTCGTGGG	1980
Q	y	1985	AGCCAGAAGCTTCCGACAGAAAAAGAGGGCCGAGCGTTCACCTCGAGGTTGAAGGCACT	2044
D	b	1981	AGCCAGAAGCTTCCGACAGAAAAAGAGGGCCGAGCGTTCACCTCGAGGTTGAAGGCACT	2040
Q	y	2045	GTTCAAGCTGTCTCAACTACGACGGGGCGGGCGCCCCGGCCCTCTGGGCGCTGTGTCT	2104
D	b	2041	GTTCAAGCTGTCTCAACTACGACGGGGCGGGCGCCCCGGCCCTCTGGGCGCTGTGTCT	2100
Q	y	2105	GGGCTTGACGATATCCACAGGGGCTGCGGCACCTTCGTGCTGCGTGTGCGGGCCCAAGA	2164
D	b	2101	GGGCTTGACGATATCCACAGGGGCTGCGGCACCTTCGTGCTGCGTGTGCGGGCCCAAGA	2160
Q	y	2165	CCCGCCGCTGAGCTGTA-----CATCCC	2188
D	b	2161	CCCGCCGCTGAGCTGTA-----CATCCC	2220
Q	y	2189	CCAGGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTTACTGCGT	2248
D	b	2221	CCAGGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTTACTGCGT	2280
Q	y	2249	GCGTCGGTATGCCGTGTGCCAAGAGCCGCCCATGCGGCACTCCGCAAGGCTTCAAGAG	2308
D	b	2281	GCGTCGGTATGCCGTGTGCCAAGAGCCGCCCATGCGGCACTCCGCAAGGCTTCAAGAG	2340
Q	y	2309	CCACGTCCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGCA	2368
D	b	2341	CCACGTCCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGCA	2400
Q	y	2369	GGAGACCAAGCCCGCTGAGGATGCCGTCGTCATCGAGACAGCTCCTCCCTGAATGAGGC	2428
D	b	2401	GGAGACCAAGCCCGCTGAGGATGCCGTCGTCATCGAGACAGCTCCTCCCTGAATGAGGC	2460
Q	y	2429	CAGCAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCCACACGCGCTGCGCATCAG	2488
D	b	2461	CAGCAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCCACACGCGCTGCGCATCAG	2520
Q	y	2489	GGGCAAGTCTACGTCACAGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCT	2548
D	b	2521	GGGCAAGTCTACGTCACAGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCT	2580
Q	y	2549	CTGCAGCCTGTGCTACGGGACATGGAGAACAAAGCTGTTTGCGGGGATTGCGGGGACGG	2608
D	b	2581	CTGCAGCCTGTGCTACGGGACATGGAGAACAAAGCTGTTTGCGGGGATTGCGGGGACGG	2640
Q	y	2609	GCTGCTCCTGCGTTTGGTGGATGATTTCTGTGTTGGTGACACCTCACCTCACCCACGCGAA	2668
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RESULT 10
US-08-911-312-1
Sequence 1, Application US/08911312
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 782..4177
; OTHER INFORMATION: /product= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hTERT)"
; OTHER INFORMATION: /note= "CDNA contained in plasmid
; OTHER INFORMATION: pGRN121"
US-08-911-312-1

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Query Match	99.18;	Score 3970;	DB 13;	Length 7029;
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QY	366	GCGCTGCTGACGGGGCCCCCGGGGGCCCCCCCCCGAGGCTTCACCACCAGCGTGGCAGC	425
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QY	486	CGCGCGTGGGCGACGACGTGCTGTTACACTGTGTGCACGCTGCGGCTCTTTGTGCTG	545
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APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312A
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elmhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7029 base pairs
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TOPOLOGY: linear
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OTHER INFORMATION: /product= "human telomerase reverse
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US-08-911-312A-1

Query Match 99.1%; Score 3970; DB 13; Length 7029;
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Matches.3980; Conservative 0; Mismatches 1; Indels 36; Gaps 1;

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Db 3065 CACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGAGACAGTTCGTGGCTCACTGCA 3124
QY 2370 GAGACCAAGCCGCTGAGGGATGCGGTGTCATGACAGCAGAGCTCTCCGTGAATGAGGCC 2429
Db 3125 GAGACCAAGCCGCTGAGGGATGCGGTGTCATGACAGCAGAGCTCTCCGTGAATGAGGCC 3184
QY 2430 AGCAGTGGCCTTTCGAGCTCTCCACGCTTCATGTGCCACACGCGCGTGGCATCAGG 2489
Db 3185 AGCAGTGGCCTTTCGAGCTCTCCACGCTTCATGTGCCACACGCGCGTGGCATCAGG 3244
QY 2490 GGCAGTCTCTACGTCAGTGCAGGGGATCCCGCAGGCTCCATCTCTCCACGCTGCTC 2549
Db 3245 GGCAGTCTCTACGTCAGTGCAGGGGATCCCGCAGGCTCCATCTCTCCACGCTGCTC 3304
QY 2550 TGCAGCCTGTGCTACGGGCAATGAGAACAGAGCTGTTGCGGGGATTCGGGGGAGCGG 2609
Db 3305 TGCAGCCTGTGCTACGGGCAATGAGAACAGAGCTGTTGCGGGGATTCGGGGGAGCGG 3364
QY 2610 CTGCTCTGCGCTTGTGTGATGATTTCTTGTGTGACACACCTCACTCAACCCAGCGAAA 2669
Db 3365 CTGCTCTGCGCTTGTGTGATGATTTCTTGTGTGACACACCTCACTCAACCCAGCGAAA 3424
QY 2670 ACCTTCTCAGGACCCCTGTCGAGGTGTCCTGAGTATGGCTGCTGTGAACCTTGGCG 2729
Db 3425 ACCTTCTCAGGACCCCTGTCGAGGTGTCCTGAGTATGGCTGCTGTGAACCTTGGCG 3484
QY 2730 AAGACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGACAGGCTTTGTTTCA 2789
Db 3485 AAGACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGACAGGCTTTGTTTCA 3544
QY 2790 ATGCCGGCCACGGCCATATCCCTGGTGGCGGCTGCTGTGATACCCGGACCTGGAG 2849
Db 3545 ATGCCGGCCACGGCCATATCCCTGGTGGCGGCTGCTGTGATACCCGGACCTGGAG 3604
QY 2850 GTGCAGAGGCACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACTTCAAC 2909
Db 3605 GTGCAGAGGCACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACTTCAAC 3664
QY 2910 CGCGGCTTCAAGGCTGGAGGAACATGCGTCCGAACCTTTGGGGTCTTGGCGTGAAG 2969
Db 3665 CGCGGCTTCAAGGCTGGAGGAACATGCGTCCGAACCTTTGGGGTCTTGGCGTGAAG 3724
QY 2970 TGTACAGGCTGTTTCTGTGATTTGCAGGTGAACAGGCTCCAGAGCGTGTGACCAACATC 3029
Db 3725 TGTACAGGCTGTTTCTGTGATTTGCAGGTGAACAGGCTCCAGAGCGTGTGACCAACATC 3784
QY 3030 TACAAGATCTCTCTGCTGACGGCGTACAGGTTTACAGCATGTGTGCTGCAGCTCCATT 3089
Db 3785 TACAAGATCTCTCTGCTGACGGCGTACAGGTTTACAGCATGTGTGCTGCAGCTCCATT 3844
QY 3090 CATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCAATCTGTGACAGCGGCTCC 3149
Db 3845 CATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCAATCTGTGACAGCGGCTCC 3904
QY 3150 CTCTGCTACTTCCATCTGTAAAGCCAAAGACGAGGATGTGCTGGGGGCCAAAGGGCGCC 3209
Db 3905 CTCTGCTACTTCCATCTGTAAAGCCAAAGACGAGGATGTGCTGGGGGCCAAAGGGCGCC 3964
QY 3210 GCCGGCCCTGTGCCCTCGAGGCCGTGAGTGGCTGTGCCACCAAGCATTCTGTCAAG 3269
Db 3965 GCCGGCCCTGTGCCCTCGAGGCCGTGAGTGGCTGTGCCACCAAGCATTCTGTCAAG 4024
QY 3270 CTGACTCGAACCCGTGTACCTACGTGCACTCTGTGGGGTCACTCAGACAGCCAGAGC 3329
Db 4025 CTGACTCGAACCCGTGTACCTACGTGCACTCTGTGGGGTCACTCAGACAGCCAGAGC 4084

QY	3330	CAGCTGAGTCGGAAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAACCCG	3389
Db	4085	CAGCTGAGTCGGAAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAACCCG	4144
QY	3390	GCATGCCCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCACAGCCAGGCC	3449
Db	4145	GCATGCCCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCACAGCCAGGCC	4204
QY	3450	GAGAGCAGACACCAGCAGCCCTGTACGCCGGGCTCTACGTTCCACAGGAGGAGGGGGCGG	3509
Db	4205	GAGAGCAGACACCAGCAGCCCTGTACGCCGGGCTCTACGTTCCACAGGAGGAGGGGGCGG	4264
QY	3510	CCCAACACCCAGGCCCCGACCCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTTTGGCCGAGGCC	3569
Db	4265	CCCAACACCCAGGCCCCGACCCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTTTGGCCGAGGCC	4324
QY	3570	TGCATGTCGGGCTGAAGGCTGAGTGTCGGGCTGAGGCTGAGCGAGTGTCAGCCAAAGG	3629
Db	4325	TGCATGTCGGGCTGAAGGCTGAGTGTCGGGCTGAGGCTGAGCGAGTGTCAGCCAAAGG	4384
QY	3630	CTGAGTGTCCAGCACACACCTGCCGCTTTCACCTTCCCAACAGGCTGGGCTGCCACCC	3689
Db	4385	CTGAGTGTCCAGCACACACCTGCCGCTTTCACCTTCCCAACAGGCTGGGCTGCCACCC	4444
QY	3690	CAGGGCCAGCTTTCCTCACCAGAGAGCCCGGCTTCACATCCCCACATAGGAATAGTCCAT	3749
Db	4445	CAGGGCCAGCTTTCCTCACCAGAGAGCCCGGCTTCACATCCCCACATAGGAATAGTCCAT	4504
QY	3750	CCCCAGATTGCGCATTTGTTACACCCCTGCGCCCTGCCCCCTTGTGCTTCCACCCCCACCAT	3809
Db	4505	CCCCAGATTGCGCATTTGTTACACCCCTGCGCCCTGCCCCCTTGTGCTTCCACCCCCACCAT	4564
QY	3810	CCAGGTGAGACCCCTGAGAAAGACCCCTGGGAGCTCTGGAATTGTGAGTGACCAAAAGTG	3869
Db	4565	CCAGGTGAGACCCCTGAGAAAGACCCCTGGGAGCTCTGGAATTGTGAGTGACCAAAAGTG	4624
QY	3870	TGCCCTGTACACAGGCGAGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTGGG	3929
Db	4625	TGCCCTGTACACAGGCGAGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTGGG	4684
QY	3930	GGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA	3986
Db	4685	GGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA	4741

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RESULT 12
PCT-US01-15774-3
; Sequence 3, Application PC/US0115774
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF
; FILE REFERENCE: ISPH-0568
; CURRENT APPLICATION NUMBER: PCT/US01/15774
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
PCT-US01-15774-3

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Query Match	99.1%;	Score 3969;	DB 1;	Length 4015;
Best Local Similarity	99.1%;	Pred. No. 2.1e-139;		
Matches 3979;	Conservative	0;	Mismatches 0;	Indels 36;
				Gaps 1;

QY	8	GCAGCGCTGCGTCTCTGCTGCGCAGCTGGGAAAGCCCTGGCCCCCGGCCACCCCGCGATGCC	67
Db	1	GCAGCGCTGCGTCTCTGCTGCGCAGCTGGGAAAGCCCTGGCCCCCGGCCACCCCGCGATGCC	60
QY	68	GGCGGCTCCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT	127
Db	61	GGCGGCTCCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT	120
QY	128	GCCGCTGGCCACGTTGCTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGACGGCGG	187
Db	121	GCCGCTGGCCACGTTGCTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGACGGCGG	180
QY	188	GGACCCCGCGGGCTTTCGCGCGCGCTGCTGGCCCCAGTGCCTGGTGTGCTGCCCTGGGACGC	247
Db	181	GGACCCCGCGGGCTTTCGCGCGCGCTGCTGGCCCCAGTGCCTGGTGTGCTGCCCTGGGACGC	240
QY	248	ACGGCGCCCCCGCGCGCGCCCTTCCGCCAGGTGTCTGCTGAAAGAGCTGTGGC	307
Db	241	ACGGCGCCCCCGCGCGCCCTTCCGCCAGGTGTCTGCTGAAAGAGCTGTGGC	300
QY	308	CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC	367
Db	301	CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC	360
QY	368	GCTGCTGAGCGGGGGCG	427
Db	361	GCTGCTGAGCGGGGGCG	420
QY	428	CCCGCCCAACACGCGTGACCGCAGCTGCGGGGAGCGGGCGGTGGGGGCTGCTGCTGCG	487
Db	421	CCCGCCCAACACGCGTGACCGCAGCTGCGGGGAGCGGGCGGTGGGGGCTGCTGCTGCG	480
QY	488	CCGCGTGGGGCGAGCAGCTGCTGTTCACTGCTGGCAGCGTGGCGCTCTTGTGCTGCT	547
Db	481	CCGCGTGGGGCGAGCAGCTGCTGTTCACTGCTGGCAGCGTGGCGCTCTTGTGCTGCT	540
QY	548	GCGTCCACGCTGCGCCTACCAGGTGTGCGGGCGCGCGCTGTACAGCTCGGGCGTGCAC	607
Db	541	GCGTCCACGCTGCGCCTACCAGGTGTGCGGGCGCGCGCTGTACAGCTCGGGCGTGCAC	600
QY	608	TCAGGCGCGCGCGCGCGCGCACACGCTAGTGGACCCCGAAGGCGTGGGATGCGAAGCGGC	667
Db	601	TCAGGCGCGCGCGCGCGCGCACACGCTAGTGGACCCCGAAGGCGTGGGATGCGAAGCGGC	660
QY	668	CTGGAACCATAGCGTCAGGGAGCGCGGGTCCCGCTGGGCTGCGCAGCCCCGGGTGCGAG	727
Db	661	CTGGAACCATAGCGTCAGGGAGCGCGGGTCCCGCTGGGCTGCGCAGCCCCGGGTGCGAG	720
QY	728	GAGCGCGGGGGCGAGTGCACCGCGAAGTCTGCCGTTGCCAAGAGGCCCAAGCGTGGCGC	787
Db	721	GAGCGCGGGGGCGAGTGCACCGCGAAGTCTGCCGTTGCCAAGAGGCCCAAGCGTGGCGC	780
QY	788	TGCGCCCTGAGCGCGGAGCGGACCGCCCTTGGGCAAGGGGTCTGGGCCCCCAGCGGCGAGAC	847
Db	781	TGCGCCCTGAGCGCGGAGCGGACCGCCCTTGGGCAAGGGGTCTGGGCCCCCAGCGGCGAGAC	840
QY	848	GCGTGAACCGAGTGACCGTGTCTGTGTGTGTACCTGCGCAGACCCCGCGAAGAGC	907
Db	841	GCGTGAACCGAGTGACCGTGTCTGTGTGTGTACCTGCGCAGACCCCGCGAAGAGC	900
QY	908	CACCTCTTTGGAGGGTGCCTCTGTGGCAGCGCGCCACTCCACCCATCCGCTGGGGCGCGCA	967
Db	901	CACCTCTTTGGAGGGTGCCTCTGTGGCAGCGCGCCACTCCACCCATCCGCTGGGGCGCGCA	960
QY	968	GCACCAACGGGGGGCCCCCATTCACATCGGGGGCCACCAAGTCCCTGGGACACGCGCTTGTCC	1027
Db	961	GCACCAACGGGGGGCCCCCATTCACATCGGGGGCCACCAAGTCCCTGGGACACGCGCTTGTCC	1020
QY	1028	CCGCGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGCGCAAGAGAGCAGCTGCG	1087
Db	1021	CCGCGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGCGCAAGAGAGCAGCTGCG	1080

QY	1088	GCCTCTCTTCCCTACTCAGCTCTCTGAGGCCACAGCCTGACTGCGCTCGGAGGCTCGTGGA	1147
Db	1081	GCCTCTCTTCCCTACTCAGCTCTCTGAGGCCACAGCCTGACTGCGCTCGGAGGCTCGTGGA	1140
QY	1148	GACCATCTTTCTGGGTTCCAGGCCCTGTGATGCCAGGACATCCCGCAGGTTGCCCGGCT	1207
Db	1141	GACCATCTTTCTGGGTTCCAGGCCCTGTGATGCCAGGACATCCCGCAGGTTGCCCGGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGGCCCTGTGTTCTGGAGCTGCTTGGGAACACAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGGCCCTGTGTTCTGGAGCTGCTTGGGAACACAGCGCA	1260
QY	1268	GTCGCCCTACGGGGGTGCTCTCTCAAGACGACTGCCCGCTGGAGCTGCGGTACCCACAGC	1327
Db	1261	GTCGCCCTACGGGGGTGCTCTCTCAAGACGACTGCCCGCTGGAGCTGCGGTACCCACAGC	1320
QY	1328	AGCCGGTGTCGTGCCCCGGGAGAAAGCCCAAGGGCTCTGTGCGGGCCCCCGAGGAGAGGA	1387
Db	1321	AGCCGGTGTCGTGCCCCGGGAGAAAGCCCAAGGGCTCTGTGCGGGCCCCCGAGGAGAGGA	1380
QY	1388	CACAGACCCCGCTGCGCTGTGTGACGCTGTCTCCCGCAGCAGCAGCCCTGGCAGGTGTA	1447
Db	1381	CACAGACCCCGCTGCGCTGTGTGACGCTGTCTCCCGCAGCAGCAGCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTCGTGGGGGCTGCGCTGCGCGCGCGGCTGTGTGCCCCCAGGCTCTGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGGGGGCTGCGCTGCGCGCGGCTGTGTGCCCCCAGGCTCTGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGGCTTCTCTCAGGAACACCAAGAAGTTCAATCTCCCTGGGGAGCATGCCAA	1567
Db	1501	CAACGAACGCGGCTTCTCTCAGGAACACCAAGAAGTTCAATCTCCCTGGGGAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAGAGAGCTGACGTGGAAGATAGCGTGGCGGAGCTGCGCTGTGGCTGCGCAG	1627
Db	1561	GCTCTCGCTGCAGAGAGCTGACGTGGAAGATAGCGTGGCGGAGCTGCGCTGTGGCTGCGCAG	1620
QY	1628	GAGCCCGAGGGGTTGGCTGTGTTCOCGGCCGACAGACACCGTCTGCGTAGAGATCCTGGC	1687
Db	1621	GAGCCCGAGGGGTTGGCTGTGTTCOCGGCCGACAGACACCGTCTGCGTAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCAGCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCAGCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCACGGAGACACAGTTTCAAAAAGACAGGCTCTTTTCTTACCGGAAGACTGCTGGAG	1807
Db	1741	TGTCACGGAGACACAGTTTCAAAAAGACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAAACATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAACATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCGAGCATCGGGGAAGCCAGGCCCGGCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCGAGCATCGGGGAAGCCAGGCCCGGCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCCATTTGTGAACATGGACTACGTCTGGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCCATTTGTGAACATGGACTACGTCTGGGAGC	1980
QY	1988	CAGAAACGTTCCGCGAGAGAAAAGAGGGCCGACGCTCTACCTCGAGGGTGAAGCACTGTT	2047
Db	1981	CAGAAACGTTCCGCGAGAGAAAAGAGGGCCGACGCTCTACCTCGAGGGTGAAGCACTGTT	2040
QY	2048	CAGCGTGCTCAACTACGAGCGCGGGCGGGCCCGGCTCTGGGGGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGCTCAACTACGAGCGCGGGCGGGCCCGGCTCTGGGGGCTCTGTGCTGGG	2100
QY	2108	CTTGAGCAGATATCCACAGGGCCTGGCGCACCTTGCTGTGCTGTGCGGGCCAGGACCC	2167
Db	2101	CTTGAGCAGATATCCACAGGGCCTGGCGCACCTTGCTGTGCTGTGCGGGCCAGGACCC	2160
QY	2168	GCGCGCTGAGCTGTA-----CATCCCCCA	2191

[illegible]

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Db 3241 CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAGCATTCCTGCTCAAGCT 3300
QY 3272 GACTGCACACCGGTGTACCTACGTGCCACTCTGGGGTCACTCAGAGACAGCCCAAGCGCA 3331
Db 3301 GACTGCACACCGGTGTACCTACGTGCCACTCTGGGGTCACTCAGAGACAGCCCAAGCGCA 3360
QY 3332 GCTGAGTGGAAAGCTCCCGGGAGCAGCGTGAATGAGCCACCCGCGCACAGCCCAAGCGGC 3391
Db 3361 GCTGAGTGGAAAGCTCCCGGGAGCAGCGTGAATGAGCCACCCGCGCACAGCCCAAGCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGAGTGAATGAGCCACCCGCGCACAGCCCAAGCGGC 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGTGAATGAGCCACCCGCGCACAGCCCAAGCGGC 3480
QY 3452 GAGCAGACACACGAGCCCTGTACAGCCGGGCTCTACGTCCAGAGGAGGAGGGGGCGCC 3511
Db 3481 GAGCAGACACACGAGCCCTGTACAGCCGGGCTCTACGTCCAGAGGAGGAGGGGGCGCC 3540
QY 3512 CACACCCAGGCCCGCACCCGCTGGGAGTGTGAGGCTGAGTGAATGAGTGTGGCCGAGGCGCTG 3571
Db 3541 CACACCCAGGCCCGCACCCGCTGGGAGTGTGAGGCTGAGTGAATGAGTGTGGCCGAGGCGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCCAAGGCGT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCCAAGGCGT 3660
QY 3632 GAGTGTCCAGCAGACCTGCGCTTCTACCTCCACAGGCTGGCGCTGCGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGCAGACCTGCGCTTCTACCTCCACAGGCTGGCGCTGCGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTCTCTACACAGAGCCCGGCTTCCACTCCACATAGAAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTCTCTACACAGAGCCCGGCTTCCACTCCACATAGAAATAGTCCATCC 3780
QY 3752 CCAGATTCGCCATTTGTTCACCCCTCGCCCTGCCCTTCTTGGCTTCCACCCCAACCATCC 3811
Db 3781 CCAGATTCGCCATTTGTTCACCCCTCGCCCTGCCCTTCTTGGCTTCCACCCCAACCATCC 3840
QY 3812 AGGTGAGACCCGTGAGAAGGAGCCCTGGGAGCTCTGGGAATTTGAGAGTGAACCAAGGTGTG 3871
Db 3841 AGGTGAGACCCGTGAGAAGGAGCCCTGGGAGCTCTGGGAATTTGAGAGTGAACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGCGGAGGAGCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGGG 3931
Db 3901 CCCTGTACACAGCGGAGGAGCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGGG 3960
QY 3932 GAGGTGCTGTGGAGTAAATATCTGAATATGAGTTTTCAGTTTGAATAAAAAA 3986
Db 3961 GAGGTGCTGTGGAGTAAATATCTGAATATGAGTTTTCAGTTTGAATAAAAAA 4015
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RESULT 13

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PCT-US02-14867-1
: Sequence 1, Application PC/TUS0214867
: GENERAL INFORMATION:
: APPLICANT: Geron Corporation
: APPLICANT: Jiang, Xu-Rong
: APPLICANT: Chiu, Choy-Pik
: APPLICANT: Harley, Calvin B.
: TITLE OF INVENTION: Treatment for Wounds
: FILE REFERENCE: 120/200
: CURRENT APPLICATION NUMBER: PCT/US02/14867
: PRIOR FILING DATE: 2002-05-09
: PRIOR APPLICATION NUMBER: 60/289,903
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 4015
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
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: LOCATION: (56)..(3454)
: OTHER INFORMATION:
PCT-US02-14867-1
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Query Match 99.1%; Score 3969; DB 1; Length 4015;
Best Local Similarity 99.1%; Pred. No. 2,1e-139;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
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QY 8 GCAGCGCTGCTCTGCTGCGCAGGTGGAGCCCTGGCCCCGCGCACCCCGCATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGCAGGTGGAGCCCTGGCCCCGCGCACCCCGCATGCC 60
QY 68 GCGCGCTCCCGCTGCCGAGCCGTGGCGTCCCTGCTGGCGACCACTAACCGAGTGTCT 127
Db 61 GCGCGCTCCCGCTGCCGAGCCGTGGCGTCCCTGCTGGCGACCACTAACCGAGTGTCT 120
QY 128 GCGCGTGGCCACGTTGCTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGTGTCAGCGCG 187
Db 121 GCGCGTGGCCACGTTGCTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGTGTCAGCGCG 180
QY 188 GGACCCGGCGGCTTTCCGCGCGCTGTGCGCCAGTGCCTGTGTGCTGCTGCGGACGC 247
Db 181 GGACCCGGCGGCTTTCCGCGCGCTGTGCGCCAGTGCCTGTGTGCTGCTGCGGACGC 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCTCTCCCTCCGCAAGTGTCTGCTGCAAGAGCTGTGCG 307
Db 241 ACGGCGCGCGCGCGCGCGCGCGCTCTCCCTCCGCAAGTGTCTGCTGCAAGAGCTGTGCG 300
QY 308 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCAAGAGAGCTGTGCGCTTGGCTTGC 367
Db 301 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCAAGAGAGCTGTGCGCTTGGCTTGC 360
QY 368 GCTGCTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTACACACAGCGTGCAGCTA 427
Db 361 GCTGCTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTACACACAGCGTGCAGCTA 420
QY 428 CCGCGCAACACGCGTGAACCGACGCTGCGGCGGAGCGGGCGCTGCTGCTGCG 487
Db 421 CCGCGCAACACGCGTGAACCGACGCTGCGGCGGAGCGGGCGCTGCTGCTGCG 480
QY 488 CCGCGTGGCGCAGCAGCTGTGTTACCTGTGACACGCTGCGCGCTTGTGTGCTGT 547
Db 481 CCGCGTGGCGCAGCAGCTGTGTTACCTGTGACACGCTGCGCGCTTGTGTGCTGT 540
QY 548 GCGTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCTGTACACAGCTGCGCGCTGCGAC 607
Db 541 GCGTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCTGTACACAGCTGCGCGCTGCGAC 600
QY 608 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
Db 601 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 668 CTGAACCATAGCGTCAAGGAGCGCGCGCTGCGCGCTGCGCGCGCGCGCGCGAG 727
Db 661 CTGAACCATAGCGTCAAGGAGCGCGCGCTGCGCGCTGCGCGCGCGCGCGAG 720
QY 728 GAGCGCGCGCGCGAGTGCACGCGCAAGTGTGCGCGTGGCCAGAGGCGCGAGCGCG 787
Db 721 GAGCGCGCGCGCGAGTGCACGCGCAAGTGTGCGCGTGGCCAGAGGCGCGAGCGCG 780
QY 788 TCGCCCTGAGCGCGGAGCGGAGCGCGCGTGGCGAGGGGTCTGGCGCGCGCGAGAG 847
Db 781 TCGCCCTGAGCGCGGAGCGGAGCGCGCGTGGCGAGGGGTCTGGCGCGCGAGAG 840
QY 848 GCGTGAACCGAGTGAACCGTGTGTTCTGTGTGTGTACCTGCGCAGACCGCGGAAGAGC 907
Db 841 GCGTGAACCGAGTGAACCGTGTGTTCTGTGTGTGTACCTGCGCAGACCGCGGAAGAGC 900
QY 908 CACCTCTTTGAGAGGTGCGCTCTGTGCAAGCGCGCACTCCACACCAATCCGTGGCGCGCA 967
Db 901 CACCTCTTTGAGAGGTGCGCTCTGTGCAAGCGCGCACTCCACACCAATCCGTGGCGCGCA 960
QY 968 GCACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027
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|||||
Db 961 GCACCACGGGGCCCCCAITCCATCCGCGGCCACCACGTCCTGGGACACGGCTTTGTC 1020
QY 1028 CCGGGGTGACGCGGAGAGACCAGCACTTCTCTACTCTCAGGCGACAGAGAGCACTGCG 1087
Db 1021 CCGGGGTGACGCGGAGAGACCAGCACTTCTCTACTCTCAGGCGACAGAGAGCACTGCG 1080
QY 1088 GCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGCGCTGCGAGAGCTGCTGGA 1147
Db 1081 GCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGCGCTGCGAGAGCTGCTGGA 1140
QY 1148 GACCATCTTTCTGGGTTCAGAGCCCTGCAATGCCAGGGACTCCCCGCAAGTTGCCCGCT 1207
Db 1141 GACCATCTTTCTGGGTTCAGAGCCCTGCAATGCCAGGGACTCCCCGCAAGTTGCCCGCT 1200
QY 1208 GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGGAACCAAGCGCA 1267
Db 1201 GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGGAACCAAGCGCA 1260
QY 1268 GTGCCCCCTACGGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTCGGTCACCCAGC 1327
Db 1261 GTGCCCCCTACGGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTCGGTCACCCAGC 1320
QY 1328 AGCCGGTGTCTGTCGCCCCGGGAGAAAGCCCAAGGGCTCTGTGGCGGGCCCCCGAGAGAGA 1387
Db 1321 AGCCGGTGTCTGTCGCCCCGGGAGAAAGCCCAAGGGCTCTGTGGCGGGCCCCCGAGAGAGA 1380
QY 1388 CACAGACCCCGCTGCGCTGCTGAGCTGCTCGGCACAGACAGACAGCCCTGCGAGGTGA 1447
Db 1381 CACAGACCCCGCTGCGCTGCTGAGCTGCTCGGCACAGACAGACAGCCCTGCGAGGTGA 1440
QY 1448 CGGCTTCGTGGGGGCTGCCCTGCGCGCGGCTGCTGCCCCAGGCTCTGGGGCTCCAGGCA 1507
Db 1441 CGGCTTCGTGGGGGCTGCCCTGCGCGCGGCTGCTGCCCCAGGCTCTGGGGCTCCAGGCA 1500
QY 1508 CAAAGAACGCGCTTCCCTCAGGAACACCAAGAAGTTCAATCTCCCTGGGGAAGCATGCCAA 1567
Db 1501 CAAAGAACGCGCGCTTCCCTCAGGAACACCAAGAAGTTCAATCTCCCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGGCGAG 1627
Db 1561 GCTCTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGGCGAG 1620
QY 1628 GAGCCACGAGGGTGGCTGTGTCCGGCGGACAGACACCGTCTGCTGAGAGAGATCCTGGC 1687
Db 1621 GAGCCACGAGGGTGGCTGTGTCCGGCGGACAGACACCGTCTGCTGAGAGAGATCCTGGC 1680
QY 1688 CAACTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCCTTTCTTGA 1747
Db 1681 CAACTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCCTTTCTTGA 1740
QY 1748 TGTACGAGAGACCAAGTTCATAAAGAACAGAGGCTCTTTTCTACCGGAAGAGTGTCTGAG 1807
Db 1741 TGTACGAGAGACCAAGTTCATAAAGAACAGAGGCTCTTTTCTACCGGAAGAGTGTCTGAG 1800
QY 1808 CAACTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1867
Db 1801 CAACTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTTCAGGACGATCGGGAAGCCAGGCCCTGCTGAGCTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTTCAGGACGATCGGGAAGCCAGGCCCTGCTGAGCTCCAGACTCCG 1920
QY 1928 CTTTCATCCCCAAGCCTGACGGGCTGCGCGGATTTGAAACATGAGCTACGTCGTGGAGC 1987
Db 1921 CTTTCATCCCCAAGCCTGACGGGCTGCGCGGATTTGAAACATGAGCTACGTCGTGGAGC 1980
QY 1988 CAGAAGCTTCCGAGAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT 2047
Db 1981 CAGAAGCTTCCGAGAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT 2040
QY 2048 CAGCGTGTCACTACGAGCGGGCGCGGCCCTCTCTGGGCGCTCTGTGTGGG 2107
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Db 2041 CAGCGTGTCACTACGAGAGCGGGGGCGGGCGGCCCGGCTCTCTGGGCGCTGTGTGGG 2100
QY 2108 CCTGAGAGATATCCACAGGGGCTGGCGACCTTCGTGCTGCTGTGGGGCCAGAGACC 2167
Db 2101 CCTGAGAGATATCCACAGGGGCTGGCGACCTTCGTGCTGCTGTGGGGCCAGAGACC 2160
QY 2168 GCCGCTGAGCTGA-----CATCCCCCA 2191
Db 2161 GCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCCA 2220
QY 2192 GGACAGGCTCACGGAGGTCAATCGGCAGCATCATCAAAACCCAGAACAGCTACTGCGTGGC 2251
Db 2221 GGACAGGCTCACGGAGGTCAATCGGCAGCATCATCAAAACCCAGAACAGCTACTGCGTGGC 2280
QY 2252 TCGGTATGCCGTGGTCCAGAAAGCCGCCCATG6GCAAGTCCGCAAGGCCCTTCAGAGCCA 2311
Db 2281 TCGGTATGCCGTGGTCCAGAAAGCCGCCCATG6GCAAGTCCGCAAGGCCCTTCAGAGCCA 2340
QY 2312 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGCAGGA 2371
Db 2341 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGCAGGA 2400
QY 2372 GACCAGCCGCTGAGGGATGCCGTGTCATGACAGACAGAGCTCCTCCCTGAATGAGGCCAG 2431
Db 2401 GACCAGCCGCTGAGGGATGCCGTGTCATGACAGACAGAGCTCCTCCCTGAATGAGGCCAG 2460
QY 2432 CAGTGGCCTCTTCGACGCTTCTCTACGCTTCAATGTGCCACACGCGGTGGCATCAGGG 2491
Db 2461 CAGTGGCCTCTTCGACGCTTCTCTACGCTTCAATGTGCCACACGCGGTGGCATCAGGG 2520
QY 2492 CAAGTCTACGTTCAGTGGCCAGGGGATCCCGAGGGGCTCCATCTCTCCAGGCTGCTGTG 2551
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QY 2552 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTGGCGGGATTCGGCGGAGCGGCT 2611
Db 2581 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTGGCGGGATTCGGCGGAGCGGCT 2640
QY 2612 GCTCCTGCGTTTGGTGATGATTTCTTGTGTGACACCTCAACCTCACCCACGGGAAC 2671
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QY 2672 CTTCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGGCTGCGTGTGAACCTTGGCGAA 2731
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QY 2732 GACAGTGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT 2791
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QY 2792 GCCGGCCACGCGCTAATTCCTGCTGCGGCTGCTGTGATACCCGGACCTGAGGT 2851
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QY 3092 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACACGGCTCCT 3151
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACACGGCTCCT 3180
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OY 3152 CTGCTACTCCATCCTGAAAGCCAGAACGCGGATGTGCTGGGGCCCAAGGGCGCCGC 3211
DB 3181 CTGCTACTCCATCCTGAAAGCCAGAACGCGGATGTGCTGGGGCCCAAGGGCGCCGC 3240
OY 3212 CGGCCCTCTGCCCTCCGAGGCGCTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271
DB 3241 CGGCCCTCTGCCCTCCGAGGCGCTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
OY 3272 GACTCGACACCGCTGTACCTACGTGCGCATCTCTGGGGTCACTCAGACAGCCCAAGCGCA 3331
DB 3301 GACTCGACACCGCTGTACCTACGTGCGCATCTCTGGGGTCACTCAGACAGCCCAAGCGCA 3360
OY 3332 GCTGAGTCGGAAGCTCCCGGGAGCAGCGCTGACTGCCCCCTGGAGGCCGCAACCCGGC 3391
DB 3361 GCTGAGTCGGAAGCTCCCGGGAGCAGCGCTGACTGCCCCCTGGAGGCCGCAACCCGGC 3420
OY 3392 ACTGCCCTCAGACTTCAAGACCATCTGCTGATGGCCACCCGCGCCAGAGCCGCGCA 3451
DB 3421 ACTGCCCTCAGACTTCAAGACCATCTGCTGATGGCCACCCGCGCCAGAGCCGCGCA 3480
OY 3452 GAGCAGACACGACGACCCCTGTACGCGCGCTTACGTCACAGGAGGAGGGCGCGCC 3511
DB 3481 GAGCAGACACGACGACCCCTGTACGCGCGCTTACGTCACAGGAGGAGGGCGCGCC 3540
OY 3512 CACACCCAGCGCGCACCCGCTGGAGTGTGAGGCTGAGTGTGTTGGCCGAGGCGCTG 3571
DB 3541 CACACCCAGCGCGCACCCGCTGGAGTGTGAGGCTGAGTGTGTTGGCCGAGGCGCTG 3600
OY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCCAAGGCT 3631
DB 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCCAAGGCT 3660
OY 3632 GAGTGTCCAGACACCTGCGCTTCTACCTTCCCAACAGGCTGCGGCTGCGCTCCACCCCA 3691
DB 3661 GAGTGTCCAGACACCTGCGCTTCTACCTTCCCAACAGGCTGCGGCTGCGCTCCACCCCA 3720
OY 3692 GGGCCAGCTTCTCTACACGAGGAGCGCGCTTCCACTCCCAATAGGAATAGTCCATCC 3751
DB 3721 GGGCCAGCTTCTCTACACGAGGAGCGCGCTTCCACTCCCAATAGGAATAGTCCATCC 3780
OY 3752 CGAGATTCGCAATGTTCACCCCTGCGCTTCCCTCTTGGCTTCCACCCCAACCATCC 3811
DB 3781 CGAGATTCGCAATGTTCACCCCTGCGCTTCCCTCTTGGCTTCCACCCCAACCATCC 3840
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DB 3901 CCCTGTACACAGCGAGGACCCCTGACCTGAGTGGGGTCCCTGTGGCTCAAAATTGGGGG 3960
OY 3932 GAGGTGCTGTGGAGTAAATATCTGAATATAGTTTTTCAGTTTGAATAAAAA 3986
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RESULT 14
PCT-US99-06898-1

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; Sequence 1, Application PC/TUS9906898
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: PCT/US99/06898
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14

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; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
PCT-US99-06898-1

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Query Match          99.1%; Score 3969; DB 1; Length 4015;
Best Local Similarity 99.1%; Pred. No. 2.1e-139;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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OY 8 GCAGCGCTGCTCTGCTGCGCACGTGGAGAGCCCTGGCCCCGCGCACCCCGGATGCC 67
DB 1 GCAGCGCTGCTCTGCTGCGCACGTGGAGAGCCCTGGCCCCGCGCACCCCGGATGCC 60
OY 68 GCGCGTCCCGCTGCGCGAGCGGCTGCGCTCCCTGCGCAGCCACTACCGAGGTGCT 127
DB 61 GCGCGTCCCGCTGCGCGAGCGGCTGCGCTCCCTGCGCAGCCACTACCGAGGTGCT 120
OY 128 GCGGCTGGCCAGTTCGTGCGGCGGCTGGGGCCCCAGGAGCTGGCGGCTGTGACGCGG 187
DB 121 GCGGCTGGCCAGTTCGTGCGGCGGCTGGGGCCCCAGGAGCTGGCGGCTGTGACGCGG 180
OY 188 GGACCCGGGCGCTTCCGCGGCGCTGTGCGCCAGTGCCTGTGTGGTGGCCCTGGAGCG 247
DB 181 GGACCCGGGCGCTTCCGCGGCGCTGTGCGCCAGTGCCTGTGTGGTGGCCCTGGAGCG 240
OY 248 ACGGCGCGCGCGCGCGCGCGCTCTCCGCCAGGTGTCTGCTGCTGAAGAGAGTGTGGC 307
DB 241 ACGGCGCGCGCGCGCGCGCGCTCTCCGCCAGGTGTCTGCTGCTGAAGAGAGTGTGGC 300
OY 308 CGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGGAGAGACGTGTGCTGCGCTTGGC 367
DB 301 CGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGGAGAGACGTGTGCTGCGCTTGGC 360
OY 368 GCTGCTGAGCGGGGCGCGCGGGGGCCCCAGGAGCTTACACACAGCGTGGCAGCTA 427
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OY 548 GGCTCCAGCTGCGCTTACAGAGTGTGGGGGCGCGCGCTGTACCACTGGCGCTGCCAC 607
DB 541 GGCTCCAGCTGCGCTTACAGAGTGTGGGGGCGCGCGCTGTACCACTGGCGCTGCCAC 600
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DB 601 TCAGGCGCGCGCGCGCGCACACGCTAGTGACCCCGAAGCGCTGTGGAGTGCAGCGGC 660
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Db 2941 CGGCTTCAAGCCTGGAGGAACATGCGCAAACTCTTTGGGGTCTGCGGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3031
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QY 3032 CAAGATCCTCTGCTGCTGAGGCGGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3091
Db 3061 CAAGATCCTCTGCTGCTGAGGCGGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
QY 3092 TCAGCAAGTTTGGAGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGGGCTCCCT 3151
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QY 3152 CTGCTACTTCATCTCTGAAGGCCAAGAACGAGGATGTGCTGGGGGCCAAGGGCGCGC 3211
Db 3181 CTGCTACTTCATCTCTGAAGGCCAAGAACGAGGATGTGCTGGGGGCCAAGGGCGCGC 3240
QY 3212 CGGCGCTCTGCCCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271
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Db 3361 GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCGCCAGCCACCCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGAGTGTGCGCACCCGCCACAGCCAGGCGCGA 3451
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QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3660
QY 3632 GAGTGTCCAGCACACCTGCGCTCTCACTTCCCACAGGCTGGGCTGCCACCCCA 3691
Db 3661 GAGTGTCCAGCACACCTGCGCTCTCACTTCCCACAGGCTGGGCTGCCACCCCA 3720
QY 3692 GGGCAGCTTTCTCTCACCAGAGGCGCGGCTTCCACTCCACATAGGAATAGTCCATCC 3751
Db 3721 GGGCAGCTTTCTCTCACCAGAGGCGCGGCTTCCACTCCACATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTGCCATTTGTTCAACCCCTGCGCTGCGCTTGGCTTCCACCCACCATCC 3811
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RESULT 15
PCT-US99-07097-1
; Sequence 1, Application PC/TUS9907097
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-003310PC
; CURRENT APPLICATION NUMBER: PCT/US99/07097
; EARLIER FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: US 09/128,354
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
PCT-US99-07097-1

Query Match 99.1%; Score 3969; DB 1; Length 4015;
Best Local Similarity 99.1%; Pred. No. 2.1e-139;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTCTGCTGCGCACGTGGGAAGCCCTGGGCCCGCCACCCCGGATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGCACGTGGGAAGCCCTGGGCCCGCCACCCCGGATGCC 60
QY 68 GCGGCTCCCGCTGCGGAGCGCTGCGCTCCTGCTGCGCAGCCACTACCGGAGTGTCT 127
Db 61 GCGGCTCCCGCTGCGGAGCGCTGCGCTCCTGCTGCGCAGCCACTACCGGAGTGTCT 120
QY 128 GCCGTGGCACGTTCTGTGGCGGCGCTGGGGCCCGCAGGGCTGGGGCTGTGACAGCGG 187
Db 121 GCCGTGGCACGTTCTGTGGCGGCGCTGGGGCCCGCAGGGCTGGGGCTGTGACAGCGG 180
QY 188 GGACCGCGCGCTTTCGCGCGCGCTGTGGCCAGTGCCTGTGTGCTGCCCCTGGGAGCG 247
Db 181 GGACCGCGCGCTTTCGCGCGCGCTGTGGCCAGTGCCTGTGTGCTGCCCCTGGGAGCG 240
QY 248 ACGGCGCGCGCGCGCGCGCGCTCTCTCCGCAAGTGTCTGCTGAAGAGCTGTGGC 307
Db 241 ACGGCGCGCGCGCGCGCGCGCTCTCTCCGCAAGTGTCTGCTGAAGAGCTGTGGC 300
QY 308 CCGAGTGTCAAGAGCTGTGCGAGCGCGCGCGCAAGAACGTGTGCTTGGCTTCCG 367
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QY	788	TGCCCCTAGCCCGAGCGAGCGCCCGTGGGCGAGGGGCTGGGCCACCACCCGGCGCAGAC	847
Db	781	TGCCCCTAGCCCGAGCGAGCGCCCGTGGGCGAGGGGCTGGGCCACCACCCGGCGCAGAC	840
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QY	908	CACCTCTTTGGAGGGTGGCGCTCTCTGGCAGCGGCCACTGCCACCACCTCCGTGGGCGCGCA	967
Db	901	CACCTCTTTGGAGGGTGGCGCTCTCTGGCAGCGGCCACTGCCACCACCTCCGTGGGCGCGCA	960
QY	968	GCACCACGCGGGGCCCCCATCCATCGCGGCCACACAGTCCCTGGGACACGCGCTGTGCC	1027
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QY	1028	CCCCGTGTACGCCGAGACCAAGACTTCCCTTACTCCTCAAGGCGAACAAAGAGCAGCTGGC	1087
Db	1021	CCCCGTGTACGCCGAGACCAAGACTTCCCTTACTCCTCAAGGCGAACAAAGAGCAGCTGGC	1080
QY	1088	GCCCTCTTCTACTACTCAGCTCTCTGAGGCCAGCCCTGACTGGCGCTCGAGGCTCTGTGA	1147
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QY	1148	GACCATCTTCTGTGGTTCCAGGCGCCTGGATGCCAGGACTCCCCGCAAGTTGCCCGCGCT	1207
Db	1141	GACCATCTTCTGTGGTTCCAGGCGCCTGGATGCCAGGACTCCCCGCAAGTTGCCCGCGCT	1200
QY	1208	GCCCCAGCGCTACTGCAAAATGCGGCCCGCTGTCTTCTGAGACTGCTTGGGAACCAACGCGCA	1267
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QY	1328	AGCCGCTGTCTGTGCCCGGGAAGACCCACAGGGCTCTGTTGGCGGCGCCCGAGAGGAGGA	1387
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QY	1388	CACAGACCCCCCGTGCCTGTGTGACAGCTGCTCTCCAGCACAGCAGCAGCCCTGCGCAGGTGA	1447
Db	1381	CACAGACCCCCCGTGCCTGTGTGACAGCTGCTCTCCAGCACAGCAGCAGCCCTGCGCAGGTGA	1440
QY	1448	CGGCTTGTGCGGGCGCTTGCCCTGGCGCCGCGTGGTGGCCCCCAGGGCGCTTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTGTGCGGGCGCTTGCCCTGGCGCCGCGTGGTGGCCCCCAGGGCGCTTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCCCGCTTCTCAGGAACACCAAGAAATTCACTCTCCCTGGGGAAGCATGCCAA	1567
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QY	1568	GCTCTCGTGCAGAGCTGACGTGGAAGATAGCGTGGGGGACTGGCGCTTGCTTCCGCAAG	1627
Db	1561	GCTCTCGTGCAGAGCTGACGTGGAAGATAGCGTGGGGGACTGGCGCTTGCTTCCGCAAG	1620
QY	1628	GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGACCGTCTGCGTAGAGAGATCCTGGC	1687
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGACCGTCTGCGTAGAGAGATCCTGGC	1680
QY	1688	CAAGTTCTTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTAAGTCTTTCTTTA	1747

Db	1681	CAAGTTCCTGCACACTGGCTGATGAGTGTGTACGTGCTGAGACTGCTCAGAGTCTTTCTTTTA	1740
OY	1748	TGTCACGGAGAACACACGTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAAGTGTCTGGAG	1807
Db	1741	TGTCACGGAGAACACACGTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAAGTGTCTGGAG	1800
OY	1808	CAAGTTGCAAAAGCATTTGGAATTCAGACAGACACTTGAAGAGGCTGCAGCTCCGGAGCTGTG	1867
Db	1801	CAAGTTGCAAAAGCATTTGGAATTCAGACAGACACTTGAAGAGGCTGCAGCTCCGGAGCTGTG	1860
OY	1868	GGAAGCAGAGGTGACGGCAGCATCGGGGAGAGCCAGAGCCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTGACGGCAGCATCGGGGAGAGCCAGAGCCCGCCCTGCTGACGTCCAGACTCCG	1920
OY	1928	CTTCATCCCCAAGCCTTGACGGGCTGCGGCCGATTTGTAACATGAGCTACGTCGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTTGACGGGCTGCGGCCGATTTGTAACATGAGCTACGTCGTGGAGC	1980
OY	1988	CAGAAGCTTCCGACAGAGAAAGAGAGGGCCGAGCGTCTCAGCTCGAGGGTGAAGCACTGTT	2047
Db	1981	CAGAAGCTTCCGACAGAGAAAGAGAGGGCCGAGCGTCTCAGCTCGAGGGTGAAGCACTGTT	2040
OY	2048	CAGCGTGTCTCAACTACGAGCGGGGCGCGCCCGCCCTCTGAGGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCTCAACTACGAGCGGGGCGCGCCCGCCCTCTGAGGCGCTCTGTGCTGGG	2100
OY	2108	CCTGGACGATATCCACAGAGGCGCTGGCGCACCTTCTGTCGCTGTGGGGGCCAGGACCC	2167
Db	2101	CCTGGACGATATCCACAGAGGCGCTGGCGCACCTTCTGTCGCTGTGGGGGCCAGGACCC	2160
OY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCTGAGCTGTA-----CATCCCCA	2220
OY	2192	GGACAGGCTCAGGAGGTCATCGCCAGCATTCATCAACCCAGAACACGTAAGTGGTGG	2251
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OY	2252	TGCGTATGCCGTGTGCTCCAGAAAGCGCCCATAGGGCACGTCGCCAAAGGCTTCAAGAGCCA	2311
Db	2281	TGCGTATGCCGTGTGCTCCAGAAAGCGCCCATAGGGCACGTCGCCAAAGGCTTCAAGAGCCA	2340
OY	2312	CGTCTCTACCTTGACAGACCTCCAGCCCGTACATGCGACAGATTGCTGCTCACCCTGCAGGA	2371
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCCGTACATGCGACAGATTGCTGCTCACCCTGCAGGA	2400
OY	2372	GACCAGCCCGCTGAGGGATGCCCTGCTCATGAGCAGAGAGCTCCTCCCTGAATGAGGCCAG	2431
Db	2401	GACCAGCCCGCTGAGGGATGCCCTGCTCATGAGCAGAGAGCTCCTCCCTGAATGAGGCCAG	2460
OY	2432	CAGTGGCTCTTGACAGTCTTCTCTACGCTTATGTGCCACCAAGCCGTGGCATCAGGGG	2491
Db	2461	CAGTGGCTCTTGACAGTCTTCTCTACGCTTATGTGCCACCAAGCCGTGGCATCAGGGG	2520
OY	2492	CAAGTCTACGTCACGTCGACAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTCTG	2551
Db	2521	CAAGTCTACGTCACGTCGACAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTCTG	2580
OY	2552	CAGCCTGTGCTACGGCGACATGGAAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGGCT	2611
Db	2581	CAGCCTGTGCTACGGCGACATGGAAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGGCT	2640
OY	2612	GCTCCTGGGTTTGGTGGATGATTTCTTGGTGACACCTCACCCTACCCACGCGGAAAAC	2671
Db	2641	GCTCCTGGGTTTGGTGGATGATTTCTTGGTGACACCTCACCCTACCCACGCGGAAAAC	2700
OY	2672	CTTCCTCAGGACCCGTGCTCCGAGGCTGCTCCGAGTATGGCTGCGTGGTGAACCTTCGGAA	2731
Db	2701	CTTCCTCAGGACCCGTGCTCCGAGGCTGCTCCGAGTATGGCTGCGTGGTGAACCTTCGGAA	2760
OY	2732	GACAGTGTGAACCTTCCCTGTAGAGAGCAGAGCCCTGGGTGGCAGCGCTTTTGTTCAGAT	2791

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QY 3752 CCAGATTGCCATTGTTCAACCTTGCCCTGCGCTCTTGGCTTCCACCCCCACCATCC 3811
Db 3781 CCAGATTGCCATTGTTCAACCTTGCCCTGCGCTCTTGGCTTCCACCCCCACCATCC 3840
QY 3812 AGGTGAGAGCCCTGAGAAGACCTGGAGCTCTGGGAATTTGAGTGACCAAAAGGTG 3871
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QY 3872 CCCTGTACACAGCGAGACCCCTGACCTGATGGGGTCCCTGTGGTCAAAATTGGGG 3931
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Db 3961 GAGTGTCTGGAGTAAATACTGAATATAGATTTTTCAGTTTGAAGAAAAA 4015

Search completed: April 17, 2003, 04:28:31
Job time : 8324 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2003, 14:15:49 ; Search time 797 Seconds

(without alignments)
11319.329 Million cell updates/sec

Title: US-09-424-686B-1DEL

Perfect score: 4006

Sequence: 1 gttcagcagcgcgtgctc.....aaaaaaaaaaaaaaaaaaaa 4006

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3996	99.8	4042	20	AAV72117 Human catalytic te
2	3981	99.4	4037	19	AAV22428 Human telomerase r
3	3973.8	99.2	4023	19	AAV60320 Human telomerase g
4	3969.4	99.1	4070	24	ABL53711 Human telomerase c
5	3969	99.1	4015	20	AAZ30154 CDNA encoding a hu
6	3969	99.1	4015	20	AAZ20279 Human telomerase r
7	3969	99.1	4015	20	AAZ00724 Human telomerase c
8	3969	99.1	4015	22	AAH45901 Human hTERT gene
9	3969	99.1	4015	24	ABA97534 Cancer cell discr

10	3967.4	99.0	4015	20	AAZ08150 Human telomerase r
11	3967	99.0	4027	20	AAH89424 Human EST2 coding
12	3967	99.0	4027	21	AAA29388 hEST2, a human tel
13	3914.8	97.7	3964	20	AAH18254 Human telomerase c
14	3910	97.6	3918	20	AAH18269 Telomerase coding
15	3910	97.6	3918	20	AAH18278 Telomerase coding
16	3899	97.3	3955	19	AAV22379 Human telomerase r
17	3843.4	95.9	51552	24	AAH96607 DNA encoding human
18	3797	94.8	3855	19	AAV22382 Human telomerase r
19	3738.6	93.3	3798	19	AAV27876 Human telomerase p
20	3353	83.7	3399	24	ABL51685 Human polynucleoti
21	3350	83.6	3396	22	AAH44366 Human telomerase n
22	3350	83.6	3396	22	AAH48235 Heart muscle cell
23	3350	83.6	3396	22	AAH49601 Human coding seque
24	3346.8	83.5	3396	22	AAH48266 Telomerase coding
25	3336.8	83.3	3500	20	AAH18275 Telomerase (ver. 2
26	3159	78.9	3167	20	AAH18271 Altered C-terminus
27	3159	78.9	3167	20	AAH18280 Altered C-terminus
28	3157	78.8	3203	20	AAH18268 Altered C-terminus
29	3147	78.6	3323	20	AAH18277 Telomerase coding
30	3132.4	78.2	7688	20	AAH18351 Telomerase coding
31	2992.2	74.7	7797	20	AAH18350 Truncated telomera
32	2808.4	70.1	3033	20	AAH18270 Truncated telomera
33	2808.4	70.1	3033	20	AAH18279 Truncated telomera
34	2804.8	70.0	3069	20	AAH18276 Truncated telomera
35	2804.8	70.0	3069	20	AAH18267 Truncated telomera
36	2798.6	69.9	7615	20	AAH18349 Telomerase coding
37	2792.8	69.7	2848	19	AAV27872 Human telomerase p
38	2485	62.0	2541	20	AAH18274 Truncated telomera
39	2485	62.0	2541	20	AAH18265 N-terminal truncat
40	2309.4	57.6	2357	20	AAH15923 Alternatively splic
41	2165	54.0	3346	19	AAH60321 Nucleotide sequenc
42	2117.4	52.9	2175	20	AAH15925 Human telomerase r
43	2114.8	52.8	2176	19	AAV22380 Human telomerase r
44	2037.6	50.9	2171	19	AAV22426 Human catalytic te
45	2035.6	50.8	3972	20	AAV72125

ALIGNMENTS

RESULT 1	
AAV72117	
ID	AAV72117 standard; CDNA; 4042 BP.
XX	
AC	AAV72117;
XX	
DT	24-MAY-1999 (first entry)
XX	
DE	Human catalytic telomerase sub-unit CDNA.
XX	
KW	Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;
KW	modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
KW	ageing; antisense; neoplastic cell; telomerase-related condition;
KW	tumour cell; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "catalytic telomerase subunit"
XX	
PN	WO9859040-A2.
XX	
PD	30-DEC-1998.
XX	
PF	09-JUN-1998; 98WO-EP03468.
XX	
PR	14-APR-1998; 98DE-1016496.
PR	20-JUN-1997; 97DE-1026329.
PR	26-MAR-1998; 98DE-1013274.
XX	

PA (FARB) BAYER AG.
XX
PI Hagen G, Slegmund H, Weichel W, Wick M, Zubov D;
XX
DR WPI; 1999-081276/07.
DR P-PSDB; AAW90251.
XX
PT New catalytically active subunit of human telomerase - used in the
PT modulation of telomerase activity, particularly for treating cancer
PT and ageing
PS
PS Claim 4; Fig 1; 76pp; German.
XX
CC This sequence encodes a novel human catalytic telomerase sub-unit
CC (hTC). The encoded protein can be used in screening assays to identify
CC modulators of telomerase and to treat or inhibit cellular disorders,
CC death, defects and/or other pathological processes involving telomerase,
CC particularly cancer and ageing (also suitable for this are agents that
CC stimulate, inhibit or mimic the activity of the subunit). Antisense
CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (i)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit.
XX
SQ Sequence 4042 BP; 684 A; 1364 C; 1277 G; 717 T; 0 other;

Query Match 99.8%; Score 3996; DB 20; Length 4042;
Best Local Similarity 99.1%; Pred. No. 8.5e-148;
Matches 4006; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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Db 1 GTTTCAGGCGAGCGCTGCTGCTGCTGCGACGTGGGAAGCCCTGGCCCCGCCACCCCG 60
QY 61 CGATGCCGCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGACGCACTACCGCG 120
Db 61 CGATGCCGCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGACGCACTACCGCG 120
QY 121 AGTGCTGCGCGTGCCACAGTTCGTGCGGCGCTGGGGCCCCCAGGGCTGGCGGCTGTGC 180
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Db 181 AGCGCGGGGACCCGCGGCTTCCGCGCGCTGGTGGCCAGTGCCTGGTGGCTGCCCT 240
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Db 481 TGTGCGCGCGCGTGGCGAGCAGAGTGTGCTTACCTGTGACGCTGGCGCTTTG 540
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Db 2941 TCAACCGCGCTTCAAGGCTGGAGGAAATGCGTCCAAACTCTTTGGGCTTGGCGC 3000
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QY 3025 ACATCTACAGATCCTCTGCTGACAGCGGTACAGGTTTCACGCATGTGTGCTGACAGCTCC 3084
Db 3061 ACATCTACAGATCCTCTGCTGACAGCGGTACAGGTTTCACGCATGTGTGCTGACAGCTCC 3120
QY 3085 CATTTCAATCAGCAAGTTTGGAGAAACCCACATTTTCTCTGCGCGTCATCTGTGACACGG 3144
Db 3121 CATTTCAATCAGCAAGTTTGGAGAAACCCACATTTTCTCTGCGCGTCATCTGTGACACGG 3180
QY 3145 CCTCCCTGCTACTCAATCTGAAGCCAAAGAACGACAGGATGCGCTGGGGCCCAAG 3204
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QY 3205 GCGCGCGCGCCCTTGTGCCCTCCGAGGCCGTGACGTGGCTGTGCCACCAAGCATTCCTGC 3264
Db 3241 GCGCGCGCGCCCTTGTGCCCTCCGAGGCCGTGACGTGGCTGTGCCACCAAGCATTCCTGC 3300
QY 3265 TCAAGCTGACTGCACACCGGTACACTACGTGCCACTCCTGGGCTCACTCAGACAGGCC 3324
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QY 3325 AGACGCAAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACCCA 3384
Db 3361 AGACGCAAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACCCA 3420
QY 3385 ACCGGCAGCTGCCCCAGACTTCAAGACCATCTGTGACTGATGATGCCACCGCCACAGCC 3444
Db 3421 ACCGGCAGCTGCCCCAGACTTCAAGACCATCTGTGACTGATGATGCCACCGCCACAGCC 3480
QY 3445 AGGCCGAGACGACACACAGCAGCCCTGTCAGCGCCGGCTCTAGCTCCAGGGAGGGAGG 3504
Db 3481 AGGCCGAGACGACACACAGCAGCCCTGTCAGCGCCGGCTCTAGCTCCAGGGAGGGAGG 3540
QY 3505 GCGCGGCCACACCCAGGCCCGGACCGCTGGGAGTGTGAGGCTGAGTGTGTTGGCCG 3564
Db 3541 GCGCGGCCACACCCAGGCCCGGACCGCTGGGAGTGTGAGGCTGAGTGTGTTGGCCG 3600
QY 3565 AGGCTGATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCC 3624
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Db 3661 AAGGCTGAGTGTCCAGACACCTGCCGCTTTCACCTTCCCACAGGCTGGCGCTCGGCTC 3720
QY 3685 CACCCAGGCGCAGCTTTCCTCACACGAGAGCGCGCTTCCACTCCCACATAGGAATAG 3744
Db 3721 CACCCAGGCGCAGCTTTCCTCACACGAGAGCGCGCTTTCACCTCCCACATAGGAATAG 3780
QY 3745 TCCATCCCGCAGATTCGCCATTTGTTACACCCCTGCGCCCTGCTTGTGCTTCCACCCCC 3804
Db 3781 TCCATCCCGCAGATTCGCCATTTGTTACACCCCTGCGCCCTGCTTGTGCTTCCACCCCC 3840
QY 3805 ACCATCAGGTGAGACCCCTGAGAAGAACCCCTGGAGCTCTGGGAATTTGGAGTGACCAA 3864

QY 788 TGCCCTGAGCCGAGCGGAGCCCGTTGGCCAGGGCTCTGGGCCACCCGGGAGAGAC 847
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Db 901 CACCTCTTTGAGGGTGCCTCTGTGGACGGCCACTCCACCCATCCGTGGGCCCA 960
QY 968 GCACCACGGGGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACACGCCCTTGTCC 1027
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Db 961 GCACCACGGGGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACACGCCCTTGTCC 1020
QY 1028 CCGGTTGTACGGCCGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAAGAGAGAGTGGC 1087
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Db 1021 CCGGTTGTACGGCCGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAAGAGAGAGTGGC 1080
QY 1088 GCCCTCCTTCTACTCAGCTCTCTGTAGGCCACGCTGACTGGCGCTGGAGGCTCTGTGA 1147
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Db 1081 GCCCTCCTTCTACTCAGCTCTCTGTAGGCCACGCTGACTGGCGCTGGAGGCTCTGTGA 1140
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QY 1268 GTGCCCTACGGGTGCTCCTCAAGACGCACTGCCGCTGAGCTGGGGTCAACCCAGC 1327
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QY 1388 CACAGACCCCGGTGCTGTGTGCAAGCTGTCTGCCAGCAGACAGACAGCCCTGGCAGGTGTA 1447
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Db 1501 CAACGAAAGCGGCTTCTCAGAGAACACCAAGAATTCACTCCCTGGGGAAGCATGGCAA 1560
QY 1568 GCTCTGCTGACGAGCTGACGTGGAAGATGAGCGGTGCGGACTGCGCTTGGCTGCGCAG 1627
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Db 1561 GCTCTGCTGACGAGCTGACGTGGAAGATGAGCGGTGCGGACTGCGCTTGGCTGCGCAG 1620
QY 1628 GAGCCGAGGGGTTGGCTGTGTTCCGGCCGAGAGACACCGTCTGCGTGAAGAGATCTGGC 1687
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Db 1621 GAGCCGAGGGGTTGGCTGTGTTCCGGCCGAGAGACACCGTCTGCGTGAAGAGATCTGGC 1680
QY 1688 CAAGTTCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTCTTTTA 1747
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Db 1681 CAAGTTCTGCACTGGCTGATGAGTGTGTGTACGTCGTCGAGCTGCTCAGGTCTTCTTTTA 1740
QY 1748 TGTACGAGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGATGTCTGAG 1807
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Db 1741 TGTACGAGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGCGAGTGTCTGAG 1800
QY 1808 CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTTGACGTCGGGAGCTGTC 1867
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Db 1801 CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTTGACGTCGGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAAGGCAGCATCGGGAGGAGCCGCGCCCTGCTGAGCTCCAGACTCCG 1927

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QY 1928 CTTATCCCAAGCCTGACGGGCTGCGGGCCGATTTGTAACATGACTACGTGCTGGAGC 1987
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Db 1921 CTTATCCCAAGCCTGACGGGCTGCGGGCCGATTTGTAACATGACTACGTGCTGGAGC 1980
QY 1988 CAGAAGCTCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGTTGAAGGCACTGTT 2047
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QY 2048 CAGCGTCTCACTACGAGAGCGGGGGCGGGCCCGCCCTGGGCTCTGTGCTGGG 2107
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Db 2041 CAGCGTCTCACTACGAGAGCGGGGGCGGGCCCGCCCTGGGCTCTGTGCTGGG 2100
QY 2108 CCTGACGATATCCACAGGGCCGTGGCGCACTTGTGCTGCTGTGCGGGCCAGAGACC 2167
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Db 2101 CCTGACGATATCCACAGGGCCGTGGCGCACTTGTGCTGCTGTGCGGGCCAGAGACC 2160
QY 2168 GCGGCTGAGCTGTA-----CATCCCCCA 2191
|||||
Db 2161 GCGGCTGAGCTGTA-----CATCCCCCA 2220
QY 2192 GGACAGGCTCACGAGAGTCAATGCCAGCATCAAAACCCAGAACACGTAATGCGTGGC 2251
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Db 2221 GGACAGGCTCACGAGAGTCAATGCCAGCATCAAAACCCAGAACACGTAATGCGTGGC 2280
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QY 2312 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTGTGCTCACCTGACAGGA 2371
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Db 2461 CAGTGGCTCTTGAGAGTCTTCTACGCTTCAATGTGCCACACAGCCGTGCGCATCAGGG 2520
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QY 2552 CAGCCTGTGCTACGGGACATGAGAAACAAGCTGTTTGGGGGATTCGGGGGAGACGGGCT 2611
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QY 2612 GCTCCTGCGTTTGGTGGATGATTTCTGTGGTGAACACCTCACCTCACCCACGCGAAAC 2671
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Db 2641 GCTCCTGCGTTTGGTGGATGATTTCTGTGGTGAACACCTCACCTCACCCACGCGAAAC 2700
QY 2672 CTTCTCAGGACCCCTGTGTCGAGGTGTCCCTGATATGCTGCTGCTGTAACCTTGGCGAA 2731
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QY 2732 GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT 2791
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QY 2792 GCGGGCCACGGGCTATTTCCCTGTGCGGGCTGCTGCTGTGATACCGGACCTTGAGGT 2851
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QY 2852 GCAGAGCACTACTCAGCTATGCCCCGAGCTTCATCAGAGCCAGTCACTTCAACCG 2911
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Db 2881 GCAGAGCACTACTCAGCTATGCCCCGAGCTTCATCAGAGCCAGTCACTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGAGGAACATGCGTGGCAACTCTTTGGGGTCTTGGGCTGAAGTG 2971
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Db 2941 CGGCTCAAGGCTGGAGGAGAACATGCGCTCGCAAACTCTTTGGGGTCTTGGGCTGAAGTG 3000

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Db 3001 TCACAGCCTGTTCTGGATTGTGACGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA 3060

QY 3032 CAAGATCCTCTGCTGACAGGCGTACAGGTTTACGCGCATGTGTGCTGACGCTCCATTTC 3091

Db 3061 CAAGATCCTCTGCTGACAGGCGTACAGGTTTACGCGCATGTGTGCTGACGCTCCATTTC 3120

QY 3092 TCAGCAAGTTTGAAGAAACCCACATTTTTCCTGCGGCTCATCTCTGACACGGCTCCCT 3151

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QY 3152 CTGCTACTCCATCTGAAAGCCCAAGAACGCGAGGATGTGCTGGGGGCGCAAGGGCGCCG 3211

Db 3181 CTGCTACTCCATCTGAAAGCCCAAGAACGCGAGGATGTGCTGGGGGCGCAAGGGCGCCG 3240

QY 3212 CGGCCCTCTGCGCTCCGAGGCGGTGACGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271

Db 3241 CGGCCCTCTGCGCTCCGAGGCGGTGACGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300

QY 3272 GACTCGACACCGTGTCACTACGTGCCACTCTGGGGTCACTCAGACAGCCCGACGCA 3331

Db 3301 GACTCGACACCGTGTCACTACGTGCCACTCTGGGGTCACTCAGACAGCCCGACGCA 3360

QY 3332 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGGCGCGCAACCCGCG 3391

Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGGCGCGCAACCCGCG 3420

QY 3392 ACTGCCCTGAGACTTCAAGACCATCTGAGACTGATGGCCACCCGCGCACAGCCAGCGCA 3451

Db 3421 ACTGCCCTGAGACTTCAAGACCATCTGAGACTGATGGCCACCCGCGCACAGCCAGCGCA 3480

QY 3452 GAGCAGACACGACGACGCCCTGTACAGCGCGGCTCTACGTCCACAGGAGGAGGGCGGCC 3511

Db 3481 GAGCAGACACGACGACGCCCTGTACAGCGCGGCTCTACGTCCACAGGAGGAGGGCGGCC 3540

QY 3512 CACACCCAGGCGCGCACCGCTGGGAGTCTGAGGCGCTGAGTGAAGTTTGGCCGAGGCGCTG 3571

Db 3541 CACACCCAGGCGCGCACCGCTGGGAGTCTGAGGCGCTGAGTGAAGTTTGGCCGAGGCGCTG 3600

QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGCGCTGAGGCGCTGAGGCGAGTGTCCAGCCAGGCGT 3631

Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGCGCTGAGGCGCTGAGGCGAGTGTCCAGCCAGGCGT 3660

QY 3632 GAGTGTCCAGACACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3691

Db 3661 GAGTGTCCAGACACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3720

QY 3692 GGGCCAGCTTTTCTCTACACGAGGAGCGCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3751

Db 3721 GGGCCAGCTTTTCTCTACACGAGGAGCGCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

QY 3752 CCAGATTGCCATTGTTCACCCCTGCGGCTGCGGCTCTTGCCTTCCACCCCCACCATCC 3811

Db 3781 CCAGATTGCCATTGTTCACCCCTGCGGCTGCGGCTCTTGCCTTCCACCCCCACCATCC 3840

QY 3812 AGGTGAGAGCCCTGAGAAGAGCCCTGGAGAGCTCTGGGAATTTGGAGTGAACCAAGGTGTG 3871

Db 3841 AGGTGAGAGCCCTGAGAAGAGCCCTGGAGAGCTCTGGGAATTTGGAGTGAACCAAGGTGTG 3900

QY 3872 CCCTGTACACAGGCGAGGAGCCCTGACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGGG 3931

Db 3901 CCCTGTACACAGGCGAGGAGCCCTGACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGGG 3960

QY 3932 GAGGTGCTGTGGAGTAAATACTGAATATAGATTTTTCAGTTTGAAGAAAAA 3991

Db 3961 GAGGTGCTGTGGAGTAAATACTGAATATAGATTTTTCAGTTTGAAGAAAAA 4020

QY 3992 AAAAAAAAAAAAAA 4006

Db 4021 AAAAAAAAAAAAAA 4035

RESULT 3
AAV60320
ID AAV60320 standard; cDNA; 4023 BP.

XX AC AAV60320;
XX
XX
DT 04-DEC-1998 (first entry)
XX
DE Human telomerase gene referred to as hEST2.
XX
KW Catalytic subunit; human; telomerase; telomere maintenance;
KW diagnosis; treatment; cancer; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..3458
FT /*tag= a

PN WO9837181-A2.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-US03404.
XX
PR 30-OCT-1997; 97US-0064322.
PR 20-FEB-1997; 97US-0038750.
PR 20-MAY-1997; 97US-0047151.
PR 01-AUG-1997; 97US-0054549.
PR 14-AUG-1997; 97US-0055762.
XX
PA (WHED) WHITEHEAD-INST BIOMEDICAL RES.
XX
PI Counter CM, Meyerson M, Weinberg RA;
XX
DR WPI: 1998-495367/42.
DR P-PSDB; AAW71376.
XX
PT New isolated human telomerase catalytic sub-unit gene - used to
PT develop products for increasing or reducing the life span of cells
PT such as cancer cells or transformed cells
XX
PS Claim 5; Fig 5A-B; 96pp; English.
XX
CC The present sequence encodes the catalytic subunit of a human
CC telomerase holoenzyme. Disruption of the telomerase gene alters
CC telomere maintenance. The DNA is essential for telomerase activity,
CC and the protein is physically associated with telomerase and a
CC constituent of active telomerase complex. The products can be used
CC for increasing or reducing the lifespan of cells such as cancer cells
CC or transformed cells. They can also be used in the diagnosis and
CC treatment of malignancies. In addition, cells with a longer lifespan
CC can be transplanted into or grafted onto an individual (e.g. as skin
CC grafts, as systems for delivery of therapeutic proteins, such as hormones
CC and enzymes), to whom they provide therapeutic benefit.
XX
SQ Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 other;

Query Match 99.2%; Score 3973.8; DB 19; Length 4023;
Best Local Similarity 99.1%; Pred. No. 6.1e-147;
Matches 3985; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

QY 5 CAGGACGCGCTGCGTCTGCTGCGGACGTTGGGAAGCCCTGGCCCGGCCACCCCGCGAT 64

Db 1 CAGGACGCGCTGCGTCTGCTGCGGACGTTGGGAAGCCCTGGCCCGGCCACCCCGCGAT 60

QY 65 GCCCGCGCTCCCGCGTGGCGAGCGGTGCGCTCCCTGCTGCGGACGCACTACCGCGAGGT 124

Db 61 GCCCGCGCTCCCGCGTGGCGAGCGGTGCGCTCCCTGCTGCGGACGCACTACCGCGAGGT 120

QY 125 GCTGCCGCTGGCCACGTTCTGTGGCGCGCTGGGGGCCCCAGGCGCTGGCGGTGTGACGG 184

[illegible]

Db	1201	CTGCCCCAGCGCTACTTGGCAAAATGCGGCCCTGTTTCTTGAGAGCTGCTTGGGAACCAACGC	1260
QY	1265	GCAGTGCCTTACGGGGTGTCTCTTCAAGACGCACTGCCGCTGCGAGCTGCGGTCAACCC	1324
Db	1261	GCAGTGCCTTACGGGGTGTCTCTTCAAGACGCACTGCCGCTGCGAGCTGCGGTCAACCC	1320
QY	1325	AGCAGCCGCTGTCTGTGCCCGGGAGAAGCCCAAGGCTGTGTGGCGGCCCCGAGAGGA	1384
Db	1321	AGCAGCCGCTGTCTGTGCCCGGGAGAAGCCCAAGGCTGTGTGGCGGCCCCGAGAGGA	1380
QY	1385	GGACACAGAACCCCGCTGCGCTGTGTGCAGCTGTCTCCGACAGCACAGCAAGCCCTGTGCAGGT	1444
Db	1381	GGACACAGAACCCCGCTGCGCTGTGTGCAGCTGTCTCCGACAGCACAGCAAGCCCTGTGCAGGT	1440
QY	1445	GTACGGCTGTGTGGGGCTGTGCTGCGCGCCGCTGTGTGCCCCAGGCGCTGTGGGCTCCAG	1504
Db	1441	GTACGGCTGTGTGGGGCTGTGCTGCGCGCCGCTGTGTGCCCCAGGCGCTGTGGGCTCCAG	1500
QY	1505	GCACAACGAACGCCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAACATGC	1564
Db	1501	GCACAACGAACGCCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAACATGC	1560
QY	1565	CAAGCTCTTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGGC	1624
Db	1561	CAAGCTCTTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGGC	1620
QY	1625	CAGGAGCCAGGGGTGTGCTGTCTCCGCGCCAGAGCACCGTCTGCGGTGAGAGATCCT	1684
Db	1621	CAGGAGCCAGGGGTGTGCTGTCTCCGCGCCAGAGCACCGTCTGCGGTGAGAGATCCT	1680
QY	1685	GGCCAAGTTCCTGCACTGCGCTGATGATGATGTGTACGTGCTGCAGCTGCTCAGTCTTCTCT	1744
Db	1681	GGCCAAGTTCCTGCACTGCGCTGATGATGATGTGTACGTGCTGCAGCTGCTCAGTCTTCTCT	1740
QY	1745	TTATGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAGAAGATGTCTG	1804
Db	1741	TTATGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAGAAGATGTCTG	1800
QY	1805	GAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAAGGTTGACGCTGCGGGAGCT	1864
Db	1801	GAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAAGGTTGACGCTGCGGGAGCT	1860
QY	1865	GTCGGAACGAGAGGTACAGGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACT	1924
Db	1861	GTCGGAACGAGAGGTACAGGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACT	1920
QY	1925	CCGCTTTCATCCCAAGCCTGACGGGCTGCGCGCGATTGTGAACATGACATACGTCTGTGG	1984
Db	1921	CCGCTTTCATCCCAAGCCTGACGGGCTGCGCGCGATTGTGAACATGACATACGTCTGTGG	1980
QY	1985	AGCCAGAAGCTTCCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTTGAAGGCACCT	2044
Db	1981	AGCCAGAAGCTTCCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTTGAAGGCACCT	2040
QY	2045	GTTTCAGCGTCTCAACTACAGAGCGGGCGCGCGGCCCGCTCCTGTGGCGCTCTGTGCT	2104
Db	2041	GTTTCAGCGTCTCAACTACAGAGCGGGCGCGCGGCCCGCTCCTGTGGCGCTCTGTGCT	2100
QY	2105	GGGCGCTGGAAGATATTCACAGGGCGCTGGCGCACTTCGTGCTGCGTGTGCGGGGCCAAGGA	2164
Db	2101	GGGCGCTGGAAGATATTCACAGGGCGCTGGCGCACTTCGTGCTGCGTGTGCGGGGCCAAGGA	2160
QY	2165	CCGCGCGCTGAGCTGTA-----CATCCC	2188
Db	2161	CCGCGCGCTGAGCTGTA-----CATCCC	2220
QY	2189	CCAGGACAGGCTACAGGAGGTATTCAGAGCTCCAGCATCATCAAAACCCAGAACACGTACTGCGT	2248
Db	2221	CCAGGACAGGCTACAGGAGGTATTCAGAGCTCCAGCATCATCAAAACCCAGAACACGTACTGCGT	2280
QY	2249	GCGTCGATATGCGGTGCTCAGAGAAGCGCCCATGCGGACGTCCGGAAGGCTTCAAGAG	2308
Db	2281	GCGTCGATATGCGGTGCTCAGAGAAGCGCCCATGCGGACGTCCGGAAGGCTTCAAGAG	2340

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QY 2309 CCACGCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCA 2368
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Db 2341 CCACGCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCA 2400
QY 2369 GGAGACCAGCCCGCTGAGGATGCCGTCGTCATCGACAGACAGCTCCTCCCTGAATAGGC 2428
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Db 2401 GGAGACCAGCCCGCTGAGGATGCCGTCGTCATCGACAGACAGCTCCTCCCTGAATAGGC 2460
QY 2429 CAGCAGTGGCTCTTCGAGCTCTCTACGCTTCATGTGCCACCAGCCGCTGCCATCAG 2488
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QY 2489 GGGCAAGTCTACGTCACGTCCAGTCCAGGGATCCCGCAGGGCTCCATCCTCTCCAGCTGCT 2548
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QY 2549 CTGCAGCCTGTGTACGCGGACATGAGAACAAAGCTGTTGCGGGGATTCGGCGGAGCG 2608
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QY 2609 GCTGCTCCTGCGTTGTGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCAGCGAA 2668
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QY 2669 AACCTTCTCAGGACCCGTGTCGAGGTGTCCCTGAGTATGGCTGCGTGTGAACCTTCCG 2728
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Db 2701 AACCTTCTCAGGACCCGTGTCGAGGTGTCCCTGAGTATGGCTGCGTGTGAACCTTCCG 2760
QY 2729 GAAGACAGTGGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGACAGGCTTTTGTCA 2788
      |||||
Db 2761 GAAGACAGTGGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGACAGGCTTTTGTCA 2820
QY 2789 GATGCCGGCCACGGCCTATTTCCCTGTGTGCGGCTGTGTGATACCCGGAGCCTTGA 2848
      |||||
Db 2821 GATGCCGGCCACGGCCTATTTCCCTGTGTGCGGCTGTGTGATACCCGGAGCCTTGA 2880
QY 2849 GGTGCAGAGCGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCTTCAA 2908
      |||||
Db 2881 GGTGCAGAGCGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCTTCAA 2940
QY 2909 CCGCGGCTTCAAGGCTGGAGGAACATGCGTCGAAACTCTTTGGGCTTTGGCGTGAA 2968
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Db 2941 CCGCGGCTTCAAGGCTGGAGGAACATGCGTCGAAACTCTTTGGGCTTTGGCGTGAA 3000
QY 2969 GTGTACAGCCTGTTTCTGATTTGACAGGTGAACAGCCTCCAGACGGTGTGCACCAACAT 3028
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QY 3029 CTACAAGATCCTCTGCTGACGAGCGGTACAGGTTTACGCATGTGTGCTGACAGCTCCATT 3088
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Db 3061 CTACAAGATCCTCTGCTGACGAGCGGTACAGGTTTACGCATGTGTGCTGACAGCTCCATT 3120
QY 3089 TCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGGCCTC 3148
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Db 3121 TCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGGCCTC 3180
QY 3149 CCTCTGCTACTCCATCTGAAGCCAAAGACGACGAGATGTGCTGGGGCCAAAGGCGC 3208
      |||||
Db 3181 CCTCTGCTACTCCATCTGAAGAACCCAAAGACGAGATGTGCTGGGGCCAAAGGCGC 3240
QY 3209 CGCCGGCCCTCTGCCCTCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTTCTGCTCAA 3268
      |||||
Db 3241 CGCCGGCCCTCTGCCCTCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTTCTGCTCAA 3300
QY 3269 GCTGACTGACACCGGTGACCTACGTGCCACTCTGCGGTCACTCAGGACAGCCAGAC 3328
      |||||
Db 3301 GCTGACTGACACCGGTGACCTACGTGCCACTCTGCGGTCACTCAGGACAGCCAGAC 3360
QY 3329 GCAGCTGAGTCGAAAGTCCCGGGGACGACGCTGACTGCCCTGGAGGCGCGACGCCAACCC 3388
      |||||
Db 3361 GCAGCTGAGTCGAAAGTCCCGGGGACGACGCTGACTGCCCTGGAGGCGCGACGCCAACCC 3420
```

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QY 3389 GGCACCTGCCCTCAGACTTCAAGACCATCCTGTGACTGATGGCCACCCGCCACAGCCAGGC 3448
      |||||
Db 3421 GGCACCTGCCCTCAGACTTCAAGACCATCCTGTGACTGATGGCCACCCGCCACAGCCAGGC 3480
QY 3449 CGAGAGCAGACACCAGACGCCCTGTACAGCCCGGCTCTACGTCCAGGAGGAGGGCGC 3508
      |||||
Db 3481 CGAGAGCAGACACCAGACGCCCTGTACAGCCCGGCTCTACGTCCAGGAGGAGGGCGC 3540
QY 3509 GCCACACCCAGGCCCGCACCCGCTGGAGTCTGAGGCCCTGAGTGTGTTGGCGAGGC 3568
      |||||
Db 3541 GCCACACCCAGGCCCGCACCCGCTGGAGTCTGAGGCCCTGAGTGTGTTGGCGAGGC 3600
QY 3569 CTGCATGTCCCGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGGAGTGTCCAGCCAAAG 3628
      |||||
Db 3601 CTGCATGTCCCGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGGAGTGTCCAGCCAAAG 3660
QY 3629 GCTGAGTGTCCAGACACACTGCCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACC 3688
      |||||
Db 3661 GCTGAGTGTCCAGACACACTGCCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACC 3720
QY 3689 CCAGGGCCAGCTTTCTCACCAGAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCA 3748
      |||||
Db 3721 CCAGGGCCAGCTTTCTCACCAGAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCA 3780
QY 3749 TCCCCAGATTCGCCATTTGTCAACCCCTGCCCCCTGCCCTTCTTCCCTCCACCCACCA 3808
      |||||
Db 3781 TCCCCAGATTCGCCATTTGTCAACCCCTGCCCCCTGCCCTTCTTCCCTCCACCCACCA 3840
QY 3809 TCCAGGTGAGACCCCTGAGAAAGACCCTGGAGCTGTGGAAATTTGAGTGAACCAAGGT 3868
      |||||
Db 3841 TCCAGGTGAGACCCCTGAGAAAGACCCTGGAGCTGTGGAAATTTGAGTGAACCAAGGT 3900
QY 3869 GTGCCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGTCAATTGG 3928
      |||||
Db 3901 GTGCCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGTCAATTGG 3960
QY 3929 GGGGAGGTGCTGTGGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 3988
      |||||
Db 3961 GGGGAGGTGCTGTGGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4020
QY 3989 AAA 3991
      |||
Db 4021 AAA 4023

RESULT 4
ABL53711
ID ABL53711 standard; cDNA; 4070 BP.
XX
AC ABL53711;
XX
DT 17-JUN-2002 (first entry)
XX
DE Human telomerase catalytic subunit hTERT cDNA.
XX
KW hTERT; telomerase; reverse transcriptase; immortalisation; human;
KW vaccine; enzyme; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200216555-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-GB03726.
XX
PR 17-AUG-2000; 2000GB-0020246.
XX
PR 17-AUG-2000; 2000US-225734P.
XX
PA (UYMA-) UNIV WALES COLLEGE OF MEDICINE.
XX
PI Jones CJ, Kipling DG, Wilkinson G, McSharry B, Skinner JW;
XX
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DR WPI: 2002-315462/35.
XX Novel hTERT-immortalized cell line (human telomerase reverse
PT transcriptase) useful for human vaccine production and preparation of
PT antigen, such as a virus or virus-derived agent -
XX
PS Example 1; Fig 1; 64pp; English.
XX
CC The present sequence is that of hTERT cDNA in plasmid pGRN121.
CC hTERT is the catalytic subunit of human telomerase. Claimed
CC immortalised cell lines for use in vaccine production are adapted
CC to express hTERT. Suitable cell lines comprise human diploid
CC fibroblasts, e.g. MRC-5 or WI38 cells, transfected with hTERT cDNA
CC or infected by a retrovirus carrying hTERT cDNA, and are capable
CC of supporting antigen production. A method for preparing such cell
CC lines using recombinant techniques is provided. The cell lines
CC are also used as a diagnostic test for the presence of a virus,
CC such as human cytomegalovirus, and to determine the efficacy of
CC antiviral agents by testing the capability of a modified virus
CC containing a reporter gene to infect the cells. The cell lines
CC have the ability, which can be impaired in cell lines immortalised
CC by other methods, of being able to support viral replication.
CC The cells remain morphologically suitable for viral/vaccine
CC cultivation.
XX
SQ Sequence 4070 BP; 670 A; 1383 C; 1296 G; 721 T; 0 other;

Query Match 99.1%; Score 3969.4; DB 24; Length 4070;
Best Local Similarity 99.1%; Pred. No. 9e-147;
Matches 3980; Conservative 0; Mismatches 1; Indels 36; Gaps 1;

QY 6 AGGCAGCGCTGCGTCTCTCTGCGCAGCTGGAGAGCCCTGGCCCGCACACCCCGCGATG 65
Db 19 ACGCAGCGCTGCGTCTCTCTGCGCAGCTGGAGAGCCCTGGCCCGCACACCCCGCGATG 78
QY 66 CCGCGCGTCCCGGCTGCGGAGCGCTGCTGCTGCTGCGCAGCCACTACCGGAGGTG 125
Db 79 CCGCGCGTCCCGGCTGCGGAGCGCTGCTGCTGCTGCGCAGCCACTACCGGAGGTG 138
QY 126 CTGCCGCTGGCAGCTGCTGCTGCGGCGCTGGGCGCCAGGGCTGGCGGTGTGTGACAGCGC 185
Db 139 CTGCCGCTGGCAGCTGCTGCTGCGGCGCTGGGCGCCAGGGCTGGCGGTGTGTGACAGCGC 198
QY 186 GGGGACCCGGGGCTTCCGGCGGCTGTGGCCCACTGCTGTGTGCTGCTGGGAC 245
Db 199 GGGGACCCGGGGCTTCCGGCGGCTGTGGCCCACTGCTGTGTGCTGCTGGGAC 258
QY 246 GCACGGCGCCCGCCCGCCCGCTTCCGCCAGGTGTCTGCTGGAAGAGCTGTG 305
Db 259 GCACGGCGCCCGCCCGCCCGCTTCCGCCAGGTGTCTGCTGGAAGAGCTGTG 318
QY 306 GCCCGAGTGTGACAGGCTGTGCGAGCGGGCGCGCAAGACGTGCTGGCTTGGCTTC 365
Db 319 GCCCGAGTGTGACAGGCTGTGCGAGCGGGCGCGCAAGACGTGCTGGCTTGGCTTC 378
QY 366 GCGCTGCTGAGCGGGGCGCGGGGCGCCCGCGAGGCTTACCAACAGCGTGGCGAGC 425
Db 379 GCGCTGCTGAGCGGGGCGCGGGGCGCCCGCGAGGCTTACCAACAGCGTGGCGAGC 438
QY 426 TACCTGCCCAACACAGGTGACCGACGCTGCGGGGAGCGGGGCTGGGGCTGTGCTG 485
Db 439 TACCTGCCCAACACAGGTGACCGACGCTGCGGGGAGCGGGGCTGGGGCTGTGCTG 498
QY 486 CGCCGCGTGGCGAGCAGCTGCTGCTTCACTGCTGCGACGCTGGCGCTCTTTGTGCTG 545
Db 499 CGCCGCGTGGCGAGCAGCTGCTGCTTCACTGCTGCGACGCTGGCGCTCTTTGTGCTG 558
QY 546 GTGGCTCCCACTGCGCTTACCAAGGTGTGCGGGCGCGCTGTACCAAGCTGGCGCTGCC 605
Db 559 GTGGCTCCCACTGCGCTTACCAAGGTGTGCGGGCGCGCTGTACCAAGCTGGCGCTGCC 618
QY 606 ACTCAGGCGCGCGCCCGCCACACGCTAGTGAGCCCGAAGGCGTCTGGGATGCGAAGCG 665
|||||

Db 619 ACTCAGGCGCGCGCCCGCCACACGCTAGTGAGCCCGCAAGGCGTCTGGGATGCGAAGCG 678
QY 666 GCGTGAACCATATAGCGTCAGAGGAGCGCGGCGTCCCGCTGGGCTGTGCCAGCCCGGCTGCG 725
Db 679 GCGTGAACCATATAGCGTCAGAGGAGCGCGGCGTCCCGCTGGGCTGTGCCAGCCCGGCTGCG 738
QY 726 AGGAGGCGCGGGGCGAGTGTCCAGCCGAGCTGTGCCGTTGCCCAAGAGGCCAGGCGTGGC 785
Db 739 AGGAGGCGCGGGGCGAGTGTCCAGCCGAGCTGTGCCGTTGCCCAAGAGGCCAGGCGTGGC 798
QY 786 GGTGCGCCCTGAGCCCGAGCGAGCGCCCGTTGGGACGGGCTCTGGGCCACCCGCGGACAG 845
Db 799 GGTGCGCCCTGAGCCCGAGCGAGCGCCCGTTGGGACGGGCTCTGGGCCACCCGCGGACAG 858
QY 846 ACGGCTGACCGAGTACCGGTGTTCTGTGTGTGTCACTGCGCAGACCCCGCGAAGAA 905
Db 859 ACGGCTGACCGAGTACCGGTGTTCTGTGTGTGTGTCACTGCGCAGACCCCGCGAAGAA 918
QY 906 GCGACCTCTTTGGAGGGTGGCGCTCTGTGGCAGCGCGCACCTCCACCCATCCGTGGCGCG 965
Db 919 GCGACCTCTTTGGAGGGTGGCGCTCTGTGGCAGCGCGCACCTCCACCCATCCGTGGCGCG 978
QY 966 CAGCACCACGCGGGCGCCCGCATCCACATGTGCGGCGCACACGTCCTCTGGGACACGCTTGT 1025
Db 979 CAGCACCACGCGGGCGCCCGCATCCACATGTGCGGCGCACACGTCCTCTGGGACACGCTTGT 1038
QY 1026 CCGCCGCTGATGCCCGAGACCAAGCACTTCTCTACCTCAGGGGACCAAGAGCAGCTG 1085
Db 1039 CCGCCGCTGATGCCCGAGACCAAGCACTTCTCTACCTCAGGGGACCAAGAGCAGCTG 1098
QY 1086 CGGCGCTCTTCTCTACTACGCTCTGTGAGGCGCCAGCGCTGACTGGCGCTGGAGGCTGTG 1145
Db 1099 CGGCGCTCTTCTCTACTACGCTCTGTGAGGCGCCAGCGCTGACTGGCGCTGGAGGCTGTG 1158
QY 1146 GAGACCATCTTCTGTGGGTGCCAGGCCCTGATGCCAGGAGACTCCCGCAGGTGCGCCCGC 1205
Db 1159 GAGACCATCTTCTGTGGGTGCCAGGCCCTGATGCCAGGAGACTCCCGCAGGTGCGCCCGC 1218
QY 1206 CTGCCCCAGCGGCTACTGTGGCAATGCGGCGCTGTTTGTGAGCTGTGTGGAAACACGCG 1265
Db 1219 CTGCCCCAGCGGCTACTGTGGCAATGCGGCGCTGTTTGTGAGCTGTGTGGAAACACGCG 1278
QY 1266 CAGTGGCCCTTACGGGGTGTCTCTCAAGAGCACACTGCCCGCTGGAGCTGGCGGTGACCCCA 1325
Db 1279 CAGTGGCCCTTACGGGGTGTCTCTCAAGAGCACACTGCCCGCTGGAGCTGGCGGTGACCCCA 1338
QY 1326 GCAGCCGGTGTGTGTGCGCGGGGAGAAAGCCCGAGGCTGTGTGGCGGCGCCCGAGAGAG 1385
Db 1339 GCAGCCGGTGTGTGTGCGCGGGGAGAAAGCCCGAGGCTGTGTGGCGGCGCCCGAGAGAG 1398
QY 1386 GACACAGACCCCGCTGCGCTGTGACGTGCTCCGCGACACAGACAGCCCGCTGGAGGTG 1445
Db 1399 GACACAGACCCCGCTGCGCTGTGACGTGCTCCGCGACACAGACAGCCCGCTGGAGGTG 1458
QY 1446 TACGGCTTGTGCGGGGCGCTGCTGCGCGGCTGTGTGCGCCAGGCGCTGTGGGGCTCCAGG 1505
Db 1459 TACGGCTTGTGCGGGGCGCTGCTGCGCGGCTGTGTGCGCCAGGCGCTGTGGGGCTCCAGG 1518
QY 1506 CACAACGAACGCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC 1565
Db 1519 CACAACGAACGCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC 1578
QY 1566 AAGCTCTGCTGACAGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGC 1625
Db 1579 AAGCTCTGCTGACAGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGC 1638
QY 1626 AGGAGCCCAAGGGTGGCTGTGCTCCGGCGCAGAGCACCGTCTGCGTGAAGAGATTCCTG 1685
Db 1639 AGGAGCCCAAGGGTGGCTGTGCTCCGGCGCAGAGCACCGTCTGCGTGAAGAGATTCCTG 1698
QY 1686 GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCTTCTTT 1745
Db 1699 GCCAAGTTCCTGCACTGGCTGATGAGTGTGTGTACGTCGTGAGCTGCTCAGGTCTTCTTT 1758
|||||

QY 1746 TATGTACGGAGACCAAGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 1805
 |||||||
 Db 1759 TATGTACGGAGACCAAGCTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 1818
 QY 1806 AGCAAGTTGCAAGCATTTGGAATCAGACAGACACTTGAAGAGGTTGACAGTGGGGAGCTG 1865
 |||||||
 Db 1819 AGCAAGTTGCAAGCATTTGGAATCAGACAGACACTTGAAGAGGTTGACAGTGGGGAGCTG 1878
 QY 1866 TCGGAAGCAGAGGTTGAGGCGACGATCGGGAAGCCAGCCCGCCCTGTGACGTCCAGACTC 1925
 |||||||
 Db 1879 TCGGAAGCAGAGGTTGAGGCGACGATCGGGAAGCCAGCCCGCCCTGTGACGTCCAGACTC 1938
 QY 1926 CGCTTCATCCCCAAGCCTGACGGGCTGGCGCGATTGTGAACATGAGTACTAGTGTGGGA 1985
 |||||||
 Db 1939 CGCTTCATCCCCAAGCCTGACGGGCTGGCGCGATTGTGAACATGAGTACTAGTGTGGGA 1998
 QY 1986 GCCAAGACGTTCCGACAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTG 2045
 |||||||
 Db 1999 GCCAAGACGTTCCGACAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTG 2058
 QY 2046 TTCAGCGTGTCACTACGAGCGGGCGGGCGCCCGCCCTCTGGGGCCTCTGTGCTG 2105
 |||||||
 Db 2059 TTCAGCGTGTCACTACGAGCGGGCGGGCGCCCGCCCGCCCTCTGGGGCCTCTGTGCTG 2118
 QY 2106 GGCCGTGACGATATCCACAGGGGCTGGCGCACCTTCGTGCTGTGCTGTGCGGGCCAGGAC 2165
 |||||||
 Db 2119 GGCCGTGACGATATCCACAGGGGCTGGCGCACCTTCGTGCTGTGCTGTGCGGGCCAGGAC 2178
 QY 2166 CCGCCGCTGAGCTGTA-----CATCCC 2189
 |||||||
 Db 2179 CCGCCGCTGAGCTGTA-----CATCCC 2238
 QY 2190 CAGGACAGGCTCAGCGGAGGTTCATCGCCAGCATCAAAACCCAGAAACAGTACTGCGTG 2249
 |||||||
 Db 2239 CAGGACAGGCTCAGCGGAGGTTCATCGCCAGCATCAAAACCCAGAAACAGTACTGCGTG 2298
 QY 2250 CGTCGGTATGCCGTGGTCCAGAAAGGCCGCCCAATGGGCACGTCCGCAAGGCTTCAAGAGC 2309
 |||||||
 Db 2299 CGTCGGTATGCCGTGGTCCAGAAAGGCCGCCCAATGGGCACGTCCGCAAGGCTTCAAGAGC 2358
 QY 2310 CACGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAG 2369
 |||||||
 Db 2359 CACGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAG 2418
 QY 2370 GAGACCAAGCCCGCTGAGGGGATGCCGTGCTCATTCGAGCAGAGAGTCTCTCCCTGAATGAGGCC 2429
 |||||||
 Db 2419 GAGACCAAGCCCGCTGAGGGGATGCCGTGCTCATTCGAGCAGAGAGTCTCTCCCTGAATGAGGCC 2478
 QY 2430 AGCAGTGGCTTTCGACGCTTCTTACGCTTCATGTGCCACACGCGCGTGCATCAGG 2489
 |||||||
 Db 2479 AGCAGTGGCTTTCGACGCTTCTTACGCTTCATGTGCCACACGCGCGTGCATCAGG 2538
 QY 2490 GGCAAGTCTTACGTCAGTCCAGTCCAGGGGATCCGACAGGGCTCCATCTCTCCACGCTGCTC 2549
 |||||||
 Db 2539 GGCAAGTCTTACGTCAGTCCAGTCCAGGGGATCCGACAGGGCTCCATCTCTCCACGCTGCTC 2598
 QY 2550 TGCAGCGTGTGCTACGGCGACATGAGAAACAAGCTGTTGCGGGATTCGCGGGAGACGGG 2609
 |||||||
 Db 2599 TGCAGCGTGTGCTACGGCGACATGAGAAACAAGCTGTTGCGGGATTCGCGGGAGACGGG 2658
 QY 2610 CTGCTCTGCGTTTGGTGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAA 2669
 |||||||
 Db 2659 CTGCTCTGCGTTTGGTGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAA 2718
 QY 2670 ACCTTCCTCAGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGGTGGAACCTTGCGG 2729
 |||||||
 Db 2719 ACCTTCCTCAGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGGTGGAACCTTGCGG 2778
 QY 2730 AAGACAGTGTGAACCTTCCCTGTAGAAGCAGAGGCCCTGGGTGGACGCGCTTTGTTCAG 2789
 |||||||
 Db 2779 AAGACAGTGTGAACCTTCCCTGTAGAAGCAGAGGCCCTGGGTGGACGCGCTTTGTTCAG 2838

QY 2790 ATGCGGGCCACGGCCCTATTTCCCTTGCTGCGCGCTGCTGTGATACCCGAGACCTTGAG 2849
 |||||||
 Db 2839 ATGCGGGCCACGGCCCTATTTCCCTTGCTGCGCGCTGCTGTGATACCCGAGACCTTGAG 2898
 QY 2850 GTGACAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACCTTCAAC 2909
 |||||||
 Db 2899 GTGACAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACCTTCAAC 2958
 QY 2910 CGCGCTTCAAGGCTGGAGGAACATGCTCGCAAACTTTTGGGGTCTTGGCGCTGAAG 2969
 |||||||
 Db 2959 CGCGCTTCAAGGCTGGAGGAACATGCTCGCAAACTTTTGGGGTCTTGGCGCTGAAG 3018
 QY 2970 TGTACAGCCCTGTTCTGATTTGACGTTGAACGCCCTCCAGACGCTGTGACCAACATC 3029
 |||||||
 Db 3019 TGTACAGCCCTGTTCTGATTTGACGTTGAACGCCCTCCAGACGCTGTGACCAACATC 3078
 QY 3030 TACAAGATCTCTGCTGACGGCGTACAGGTTTCAACGCATGTGTGCTGACGCTCCATT 3089
 |||||||
 Db 3079 TACAAGATCTCTGCTGACGGCGTACAGGTTTCAACGCATGTGTGCTGACGCTCCATT 3138
 QY 3090 CATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGCGTATCTCTGACAGGCGCTCC 3149
 |||||||
 Db 3139 CATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGCGTATCTCTGACAGGCGCTCC 3198
 QY 3150 CTCTGCTACTCATCTTGAAGAAACCCAGAAAGCGAGGATGTGCTGGGGGCCAAGGGCGCC 3209
 |||||||
 Db 3199 CTCTGCTACTCATCTTGAAGAAACCCAGAAAGCGAGGATGTGCTGGGGGCCAAGGGCGCC 3258
 QY 3210 GCCGGCCCTGTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAG 3269
 |||||||
 Db 3259 GCCGGCCCTGTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAG 3318
 QY 3270 CTGACTCGACACCCGCTGTCACCTACGTGCCACTCTGGGGTCACTCAGGACAGCCAGAGC 3329
 |||||||
 Db 3319 CTGACTCGACACCCGCTGTCACCTACGTGCCACTCTGGGGTCACTCAGGACAGCCAGAGC 3378
 QY 3330 CAGCTAGTGGAGAGCTCCCGGGGAGCAGACGCTGACTGCCCTGGAGGGCCGCAACCCG 3389
 |||||||
 Db 3379 CAGCTAGTGGAGAGCTCCCGGGGAGCAGACGCTGACTGCCCTGGAGGGCCGCAACCCG 3438
 QY 3390 GCACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACCCGCGCACAGCCAGGCC 3449
 |||||||
 Db 3439 GCACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACCCGCGCACAGCCAGGCC 3498
 QY 3450 GAGAGCAGACACAGCAGCCCTGTACAGCCGCGGCTTACGTCCACAGGAGGAGGGCGG 3509
 |||||||
 Db 3499 GAGAGCAGACACAGCAGCCCTGTACAGCCGCGGCTTACGTCCACAGGAGGAGGGCGG 3558
 QY 3510 CCCACACCCAGGCGCCGACCCGCTGGGAGTGTAGGCCCTGAGTGAAGTGTGGCCGAGGCC 3569
 |||||||
 Db 3559 CCCACACCCAGGCGCCGACCCGCTGGGAGTGTAGGCCCTGAGTGAAGTGTGGCCGAGGCC 3618
 QY 3570 TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGG 3629
 |||||||
 Db 3619 TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAAGG 3678
 QY 3630 CTGAGTGTCCAGACACCTGCGGCTTCACTTCCACAGGCTGGCGCTCGGCTCCACCC 3689
 |||||||
 Db 3679 CTGAGTGTCCAGACACCTGCGGCTTCACTTCCACAGGCTGGCGCTCGGCTCCACCC 3738
 QY 3690 CAGGGCAGCTTTTCTTCAACAGGAGCCCGGCTTCCACTCCCAACATAGGAATAGTCCAT 3749
 |||||||
 Db 3739 CAGGGCAGCTTTTCTTCAACAGGAGCCCGGCTTCCACTCCCAACATAGGAATAGTCCAT 3798
 QY 3750 CCCCAGATTGCGCAATTGTTCAACCCCTGCGGCTGCGCTTGTGCTTCCACCCACCAT 3809
 |||||||
 Db 3799 CCCCAGATTGCGCAATTGTTCAACCCCTGCGGCTGCGCTTGTGCTTCCACCCACCAT 3858
 QY 3810 CCAGGTGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGAACCAAGGTG 3869
 |||||||
 Db 3859 CCAGGTGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGAACCAAGGTG 3918
 QY 3870 TGCCCTGTACACAGGCGAGGAGCCCTGCACCTGATGGGGTCCCTGTGGGTCAAAATTGGG 3929

|||||
Db 3919 TGCCCTGACACAGGCGAGGACCCTGACCTGGATGGGGTCCCTGTGGGTCAAAATTGGG 3978
QY 3930 GGGAGGTGCTGTGGAGTAATAATGATATATGAGTTTTCAGTTTTCAGTAAAAA 3986
Db 3979 GGGAGGTGCTGTGGAGTAATAATACTGATATATGAGTTTTCAGTTTTCAGTAAAAA 4035
RESULT 5
AA230154
ID AA230154 standard; cDNA; 4015 BP.
AC AA230154;
XX
DT 26-JAN-2000 (first entry)
XX
DE cDNA encoding a human telomerase reverse transcriptase (TRT).
XX
KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW immunological destruction; telomerase; cancer; proliferation disease;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "telomerase reverse transcriptase"
XX
PN WO950392-A1.
XX
PD 07-OCT-1999.
XX
PE 30-MAR-1999; 99WO-US06898.
XX
PR 31-MAR-1998; 98US-0112006.
XX
PA (GERO-) GERON CORP.
XX
PI Gaeta FCA;
XX
DR WPI: 1999-610845/52.
DR P-PSDB; AAY43621.
XX
XX
PT Eliciting an in vivo immune response for prevention and treatment of
PT cancers
PS Disclosure; Fig 2; 26pp; English.
XX
CC The present sequence encodes a human telomerase reverse transcriptase
CC (TRT) polypeptide. The protein is used in the method of the invention.
CC The specification describes a method for activating a T lymphocyte,
CC comprising contacting the T lymphocyte with a dendritic cell that
CC expresses a TRT peptide in the context of a MHC class I or MHC class
CC II molecule. The protein causes induction of an in vivo immunological
CC response to telomerase activity. Cancer cells are characterized by
CC expression of endogenous TRT gene and the presence of detectable
CC telomerase activity. Therefore, by eliciting a specific immune response
CC to TRT or to TRT-expressing cells, it is possible to selectively target
CC proliferating cells for immunological destruction. The method is used
CC for eliciting an in vivo immune response to telomerase by activating
CC a T lymphocyte, and is useful for prevention and treatment of cancers and
CC other proliferation diseases/conditions.
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;
Query Match 99.1%; Score 3969; DB 20; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-147;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCTCTGCTGCGACGTTGGGAAGCCCTGGCCCGCCACCCCGCGATGCC 67
|||||

Db 1 GCAGCGCTGCTCTGCTGCGACGTTGGGAAGCCCTGGCCCGCCACCCCGCGATGCC 60
QY 68 GCGGCTCCCGCTGCGAGCCGTTGCGCTCCCTGCTGCGAGCCACTACCGAGGTGCT 127
Db 61 GCGGCTCCCGCTGCGAGCCGTTGCGCTCCCTGCTGCGAGCCACTACCGAGGTGCT 120
QY 128 GCGGCTGCGACGTTGCTGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 187
Db 121 GCGGCTGCGACGTTGCTGCGGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 188 GGAACCGGCGGCTTCCGCGCGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 247
Db 181 GGAACCGGCGGCTTCCGCGCGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 248 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 307
Db 241 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 308 CCGAGTGTGCTGAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
Db 301 CCGAGTGTGCTGAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 368 GCTGCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 427
Db 361 GCTGCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 420
QY 428 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
Db 421 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 488 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 547
Db 481 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
QY 548 GCGTCCGAGCTGCGGCTACAGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 607
Db 541 GCGTCCGAGCTGCGGCTACAGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 600
QY 608 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 667
Db 601 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 668 CTGGAACCATAGCGTCAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 727
Db 661 CTGGAACCATAGCGTCAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 720
QY 728 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
Db 721 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 788 TGCCCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 847
Db 781 TGCCCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 840
QY 848 GCGTGAACGAGTGAACGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907
Db 841 GCGTGAACGAGTGAACGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 908 CACCTTTTGGAGGGTGGCTCTCTGCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 967
Db 901 CACCTTTTGGAGGGTGGCTCTCTGCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
QY 968 GCACACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1027
Db 961 GCACACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
QY 1028 CCGGCTGAGCGGCGGAGACCAAGCACTCTCTACTCTCTAGGCGGCGGCGGCGGCGG 1087
Db 1021 CCGGCTGAGCGGCGGAGACCAAGCACTCTCTACTCTCTAGGCGGCGGCGGCGGCGG 1080
QY 1088 GCGCTCTCTCTACTCTCTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1147
Db 1081 GCGCTCTCTCTACTCTCTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140

QY 1148 GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCCGAGGTTGCCCGCCT 1207
|||||
Db 1141 GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCCGAGGTTGCCCGCCT 1200
QY 1208 GCCCCAGCGCTACTGGCAATATGCGGCCCTGTCTTGAGAGCTGCTTGGGAACCAAGCGCA 1267
|||||
Db 1201 GCCCCAGCGCTACTGGCAATATGCGGCCCTGTCTTGAGAGCTGCTTGGGAACCAAGCGCA 1260
QY 1268 GTGCCCCCTACGGGGTGCTCTCTCAAGACGCACTGCCCGCTGGCAGCTGCGGTCACCCCAGC 1327
|||||
Db 1261 GTGCCCCCTACGGGGTGCTCTCTCAAGACGCACTGCCCGCTGGCAGCTGCGGTCACCCCAGC 1320
QY 1328 AGCCGGTGTCTGTCGCCGGGAGAGCCCGAGGGCTCTGTGGCGGCCCGGAGGAGGAGA 1387
|||||
Db 1321 AGCCGGTGTCTGTCGCCGGGAGAGCCCGAGGGCTCTGTGGCGGCCCGGAGGAGGAGA 1380
QY 1388 CACAGACCCCGCTGCTGTGTGACGTCGCTCCGACAGACAGAGCCCGCTGGCAGGTGTA 1447
|||||
Db 1381 CACAGACCCCGCTGCTGTGTGACGTCGCTCCGACAGACAGAGCCCGCTGGCAGGTGTA 1440
QY 1448 CGGCTTCTGGGGGCTGCGCTGCGCGGCTGTGTGCCCCCAGGGCTCTGGGGCTCCAGGCA 1507
|||||
Db 1441 CGGCTTCTGGGGGCTGCGCTGCGCGGCTGTGTGCCCCCAGGGCTCTGGGGCTCCAGGCA 1500
QY 1508 CAACGAACCGCCGCTTCTCTCAGGAACACCAAGAATTCATCTCCCTGGGGAAGCATGCGCA 1567
|||||
Db 1501 CAACGAACCGCCGCTTCTCTCAGGAACACCAAGAATTCATCTCCCTGGGGAAGCATGCGCA 1560
QY 1568 GCTCTCGCTGCAAGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGCAG 1627
|||||
Db 1561 GCTCTCGCTGCAAGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGCAG 1620
QY 1628 GAGCCCAAGGGTTGGCTGTGTCCCGCCGAGAGCACCGCTGTGCGTGAAGAGATCCTGGC 1687
|||||
Db 1621 GAGCCCAAGGGTTGGCTGTGTCCCGCCGAGAGCACCGCTGTGCGTGAAGAGATCCTGGC 1680
QY 1688 CAAGTTCCTGCACTGGCTGATGATGTGTACGTCTGAGCTGCTCAGGTCCTTTCTTTA 1747
|||||
Db 1681 CAAGTTCCTGCACTGGCTGATGATGTGTACGTCTGAGCTGCTCAGGTCCTTTCTTTA 1740
QY 1748 TGTACGAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG 1807
|||||
Db 1741 TGTACGAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG 1800
QY 1808 CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGACAGTCGGGAGCTGTC 1867
|||||
Db 1801 CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGACAGTCGGGAGCTGTC 1860
QY 1868 GGAAGCAGAGTTCAGGCGACATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1927
|||||
Db 1861 GGAAGCAGAGTTCAGGCGACATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1920
QY 1928 CTTCATCCCCAAGCCTGACGGGCTGCGCGGATTTGTAACATGACTAGCTGCTGGAGC 1987
|||||
Db 1921 CTTCATCCCCAAGCCTGACGGGCTGCGCGGATTTGTAACATGACTAGCTGCTGGAGC 1980
QY 1988 CAGAAGCTTCGCGAGAGAAAAGAGGGCGAGCGTCTACCTGAGGGTGAAGGCACTGTT 2047
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Db 1981 CAGAAGCTTCGCGAGAGAAAAGAGGGCGAGCGTCTACCTGAGGGTGAAGGCACTGTT 2040
QY 2043 CAGCGTCTCACTACGAGCGGGCGGCCCGGCTCTGCGGCGCTCTGTGTGGG 2107
|||||
Db 2041 CAGCGTCTCACTACGAGCGGGCGGCCCGGCTCTGCGGCGCTCTGTGTGGG 2100
QY 2108 CCTGAGCATATCCACAGGGCTGGCGCACTTGTGTGTGCTGTGCGGGCCAGAGACC 2167
|||||
Db 2101 CCTGAGCATATCCACAGGGCTGGCGCACTTGTGTGTGCTGTGCGGGCCAGAGACC 2160
QY 2168 GCGGCTGAGCTGTA-----CATCCCCA 2191
|||||
Db 2161 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACCATCCCCCA 2220

QY 2192 GGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTTACTGCGTGC 2251
|||||
Db 2221 GGACAGGCTCAGGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTTACTGCGTGC 2280
QY 2252 TCGTATGCCGTGTCTCAGAAAGGCCCGCATGGGCACGTCCGCAAGGCTTCAAGAGCCA 2311
|||||
Db 2281 TCGTATGCCGTGTCTCAGAAAGGCCCGCATGGGCACGTCCGCAAGGCTTCAAGAGCCA 2340
QY 2312 CGTCTACTCTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGCTCACCTGCAGGA 2371
|||||
Db 2341 CGTCTACTCTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGCTCACCTGCAGGA 2400
QY 2372 GACCAGCCGCTGAGGGATGCCGTGTCATCCAGCAGAGAGCTCCCTCGAATGAGGCCAG 2431
|||||
Db 2401 GACCAGCCGCTGAGGGATGCCGTGTCATCCAGCAGAGAGCTCCCTCGAATGAGGCCAG 2460
QY 2432 CAGTGGCTCTTCGACGCTCTTCTACGCTTCATGTCACACACGCGGTGCGCATCAGGG 2491
|||||
Db 2461 CAGTGGCTCTTCGACGCTCTTCTACGCTTCATGTCACACACGCGGTGCGCATCAGGG 2520
QY 2492 CAAGTCTACGTCAGTGCAGGAGGATCCGCAAGGGCTCCATCTCTCCACGCTGCTGTG 2551
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Db 2521 CAAGTCTACGTCAGTGCAGGAGGATCCGCAAGGGCTCCATCTCTCCACGCTGCTGTG 2580
QY 2552 CAGCCTGTGCTACGCGGACATGAGAAACAGCTGTTTGGGGGATTCGGCGGAGCGGCT 2611
|||||
Db 2581 CAGCCTGTGCTACGCGGACATGAGAAACAGCTGTTTGGGGGATTCGGCGGAGCGGCT 2640
QY 2612 GCTCCTGCGTTGGTGGATGATTTCTGTGTGACACCTCACCTCACCCACGCGAAAAAC 2671
|||||
Db 2641 GCTCCTGCGTTGGTGGATGATTTCTGTGTGACACCTCACCTCACCCACGCGAAAAAC 2700
QY 2672 CTTCCTCAGAACCCCTGCTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAATTCGGAA 2731
|||||
Db 2701 CTTCCTCAGAACCCCTGCTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAATTCGGAA 2760
QY 2732 GACAGTGTGTAATTCCTGTGAGAAACAGAGCCCTGGGTGGCACGGCTTTGTTCAGAT 2791
|||||
Db 2761 GACAGTGTGTAATTCCTGTGAGAAACAGAGCCCTGGGTGGCACGGCTTTGTTCAGAT 2820
QY 2792 GCCGGCCACGGCTATTCCCTGTGTGCGGCTGCTGTGTGATACCCGGAACCTGAGGT 2851
|||||
Db 2821 GCCGGCCACGGCTATTCCCTGTGTGCGGCTGCTGTGTGATACCCGGAACCTGAGGT 2880
QY 2852 GCAGAGGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCAACTCAACCG 2911
|||||
Db 2881 GCAGAGGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCAACTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGGAGGAACATGCTGCAAACTCTTTGGGGTCTGCGCTGAAGTG 2971
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Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCTGCAAACTCTTTGGGGTCTGCGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGATTTGACGTGAACAGCCTCCAGAGCGGTGACCAACATCTA 3031
|||||
Db 3001 TCACAGCCTGTTTCTGATTTGACGTGAACAGCCTCCAGAGCGGTGACCAACATCTA 3060
QY 3032 CAAGATCTCTCTGCTGACAGGCTACAGTTTCACGCATGTGTCTGACGCTCCATTTC 3091
|||||
Db 3061 CAAGATCTCTCTGCTGACAGGCTACAGTTTCACGCATGTGTCTGACGCTCCATTTC 3120
QY 3092 TCAGCAAGTTTGAAGAACCACCAATTTTCTGCGGCTCATCTCTGACACGGCTCCCT 3151
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Db 3121 TCAGCAAGTTTGAAGAACCACCAATTTTCTGCGGCTCATCTCTGACACGGCTCCCT 3180
QY 3152 CTGCTACTCATCTCTGAAGCCAAAGAACGAGGATGTGCTGGGGCCAAAGGCGCGC 3211
|||||
Db 3181 CTGCTACTCATCTCTGAAGCCAAAGAACGAGGATGTGCTGGGGCCAAAGGCGCGC 3240
QY 3212 CGGCTCTGCGCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCAATCTGCTCAAGCT 3271
|||||
Db 3241 CGGCTCTGCGCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCAATCTGCTCAAGCT 3300
QY 3272 GACTGCACCGTGTCACTACGTGCGCACTCTGGGGTCACTCAGAGACAGCCAGAGCGA 3331

|||||
Db 3301 GACTCGACACCGTGTACCTACGTGCGACTCCTGGGGTCACTCAGACAGCCACGCA 3360
QY 3332 GCTGAGTCGGAAGCTCCCGGGGACGAGCGCTGACTGCCCTGGAGGCCGACCAACCCGGC 3391
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGAGCGCTGACTGCCCTGGAGGCCGACCAACCCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGAGTGAAGGCCACCCGCCACAGCCAGGCCGA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGTGAAGGCCACCCGCCACAGCCAGGCCGA 3480
QY 3452 GAGCAGACACGAGCGCCCTGTACAGCGCGGCTCTACGTCCACAGGAGGAGGGGGCGCC 3511
Db 3481 GAGCAGACACGAGCGCCCTGTACAGCGCGGCTCTACGTCCACAGGAGGAGGGGGCGCC 3540
QY 3512 CACACCCAGGCGCGCACCGCTGGAGTGTAGAGGCTGAGTGTGTCGCGAGGCCCTG 3571
Db 3541 CACACCCAGGCGCGCACCGCTGGAGTGTAGAGGCTGAGTGTGTCGCGAGGCCCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGGCT 3660
QY 3632 GAGTGTCCAGACACCTGCCGTCTTCACTTCCACAGGCTGGCGCTCGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCCGTCTTCACTTCCACAGGCTGGCGCTCGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTCTCTCACCAGGAGCCCGCTTCCACTCCCAATAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTCTCTCACCAGGAGCCCGCTTCCACTCCCAATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTCCGCAATGTTTCAACCCCTCGCCCTGCCCTTGTGCTTCCACCCCAACCATCC 3811
Db 3781 CCAGATTCCGCAATGTTTCAACCCCTCGCCCTGCCCTTGTGCTTCCACCCCAACCATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3871
Db 3841 AGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGGCGAGGACCTTGACACTGATGGGGTCCCTGTGGGTCAAAATTGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCTTGACACTGATGGGGTCCCTGTGGGTCAAAATTGGGG 3960
QY 3932 GAGGTGCTGTGGGAGTAATAATGTAATATAGTTTTTCAGTTTGAAAAAA 3986
Db 3961 GAGGTGCTGTGGGAGTAATAATGTAATATAGTTTTTCAGTTTGAAAAAA 4015

RESULT 6
AAZ20279
ID AAZ20279 standard; cDNA; 4015 BP.
XX AAZ20279;
AC
XX
DT 17-JAN-2000 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT) cDNA.
XX
KW Telomerase reverse transcriptase; human; hTERT; cell proliferation;
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers
FT CDS 56..3454
FT /*tag= a
XX
PN W09950386-A2.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99MO-US07097.
XX

PR 31-MAR-1998; 98US-0052864.
PR 03-AUG-1998; 9805-0128354.
XX
PA (GERO-) GERON CORP.
XX
PI Morin GB;
XX
DR WPI: 1999-610842/52.
DR P-PSDB; AAY32090.
XX
PT New catalytic polypeptide and polynucleotide, useful for increasing
PS catalytic activity in a cell
XX
XX Disclosure: Fig 2; 24pp; English.
CC
CC This is the nucleotide sequence of cDNA encoding human telomerase
CC reverse transcriptase (hTERT, see AAY32090). Human telomerase is a
CC target for diagnosing and treating diseases relating to cell
CC proliferation and senescence, such as cancer, or for increasing
CC the proliferative capacity of a cell. A claimed method for
CC increasing the proliferative capacity of a vertebrate cell,
CC especially a human or other mammalian cell, involves introducing
CC into the cell a recombinant hTERT polynucleotide encoding an hTERT
CC variant in which residues 192-323, 200-323, 192-271, 200-271,
CC 222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are
CC deleted. A claimed method for reducing telomerase activity in a
CC cell involves introducing a recombinant polynucleotide encoding
CC an hTERT variant having a deletion of amino acids 192-450, 560-565,
CC 637-660, 638-660, 748-764 or 1055-1071. The polynucleotides are
CC obtained by mutagenesis of the hTERT coding sequence.
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;
Query Match 99.1%; Score 3969; DB 20; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-147;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCCTGCTGCGACGTGGGAAGCCCTGGCCCCGACACCCCGCGATGCC 67
Db 1 GCAGCGCTGCCTGCTGCGACGTGGGAAGCCCTGGCCCCGCGATGCC 60
QY 68 GCGCGCTCCCCGCTCCGAGCGCGTCCCTGCTGCGCAGCCACTACCGCGAGTGTCT 127
Db 61 GCGCGTCCCGCTGCCGAGCGGTGCGTCCCTGCTGCGCAGCCACTACCGCGAGTGTCT 120
QY 128 GCGCGTCCCGCTGCTGCGCGCTGCGGCCCCAGGCGCTGGCGCTGTGACGCGCG 187
Db 121 GCGCGTCCCGCTGCTGCGCGCTGCGGCCCCAGGCGCTGGCGCTGTGACGCGCG 180
QY 188 GGACCCGGCGGCTTTCGCGCGCTGTGGGCCAGTGCTGTGTGCGTCCCTGGGACGC 247
Db 181 GGACCCGGCGGCTTTCGCGCGCTGTGGGCCAGTGCTGTGTGCGTCCCTGGGACGC 240
QY 248 ACGCGCGCCCCCGCGCGCTTCCGCGAGGTGTCTGCTGAGAGAGCTGTGGC 307
Db 241 ACGCGCGCCCCCGCGCGCTTCCGCGAGGTGTCTGCTGAGAGAGCTGTGGC 300
QY 308 CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGAAGAGTGTGCGCTTGGCTTGGC 367
Db 301 CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGAAGAGTGTGCGCTTGGCTTGGC 360
QY 368 GCTGCTGAGCGGGCGCGCGCGCGCGCGCGAGGCGCTTACACACGAGCTGGCGACTA 427
Db 361 GCTGCTGAGCGGGCGCGCGCGCGCGCGCGAGGCGCTTACACACGAGCTGGCGACTA 420
QY 428 CCGCCCAACAGGCTGACCGACCACTGCGGGGAGCGGGCGCTGCTGCTGCG 487
Db 421 CCTGCCCAACAGGCTGACCGACCACTGCGGGGAGCGGGCGCTGCTGCTGCG 480
QY 488 CCGCGTGGGCGAGCAGCTGTGCTTACCTGTGCGACGCTGGCGCTCTTGTGTGCTGT 547
Db 481 CCGCGTGGGCGAGCAGCTGTGCTTACCTGTGCGACGCTGGCGCGCTCTTGTGTGCTGT 540

QY 548 GGCTCCAGCTGCGCTACCAAGTGTGCGGGCCGCGCTGTACCACTCGCGCTGCCAC 607
|||||
Db 541 GGCTCCAGCTGCGCTACCAAGTGTGCGGGCCGCGCTGTACCACTCGCGCTGCCAC 600
QY 608 TCAGGCCCCCGCCCGCCACACGCTAAGTGAACCCGGAAGGCGTGTGGATGCGAAGCGGC 667
|||||
Db 601 TCAGGCCCCCGCCCGCCACACGCTAAGTGAACCCGGAAGGCGTGTGGATGCGAAGCGGC 660
QY 668 CTGAACCATAGCGTCAAGGAGGCGCGGGTCCCCCTGGGCTGCCAGCCCCCGGGTGGAG 727
|||||
Db 661 CTGAACCATAGCGTCAAGGAGGCGCGGGTCCCCCTGGGCTGCCAGCCCCCGGGTGGAG 720
QY 728 GAGGCGCGGGGCGAGTGGCCAGCCGAGTCTCCCGTTGCCAAGAGGCCCAAGGCGTGGCGC 787
|||||
Db 721 GAGGCGCGGGGCGAGTGGCCAGCCGAGTCTCCCGTTGCCAAGAGGCCCAAGGCGTGGCGC 780
QY 788 TGCCCTGAGCCGGAGCGGAGCGCCGTTGGGCAGGGGTCTGGGCCCCAGCGGCGAGAC 847
|||||
Db 781 TGCCCTGAGCCGGAGCGGAGCGCCGTTGGGCAGGGGTCTGGGCCCCAGCGGCGAGAC 840
QY 848 GCGTGGACCAAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
|||||
Db 841 GCGTGGACCAAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTTGAGAGGGGTGCGCTCTGTGGCAGCGGCCACTCCACCCATCCGTGGCGGCCA 967
|||||
Db 901 CACCTCTTTGAGAGGGGTGCGCTCTGTGGCAGCGGCCACTCCACCCATCCGTGGCGGCCA 960
QY 968 GCACACAGCGGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGCGTTGTCC 1027
|||||
Db 961 GCACACAGCGGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGCGTTGTCC 1020
QY 1028 CCGGCTGAGCGCCGAGACCAAGCACTTCCTACTCTCAGGCGACAAAGAGCAGCTGCG 1087
|||||
Db 1021 CCGGCTGAGCGCCGAGACCAAGCACTTCCTACTCTCAGGCGACAAAGAGCAGCTGCG 1080
QY 1088 GCCCTCCTCTACTACTAGCTCTGTAGGCGCCAGCGCTGACTGGCGTCGAGAGGCTCGTGA 1147
|||||
Db 1081 GCCCTCCTCTACTACTAGCTCTGTAGGCGCCAGCGCTGACTGGCGTCGAGAGGCTCGTGA 1140
QY 1148 GACCATCTTCTGTGGGTTCAGAGGCCCTGAGTGCAGGGACTCCCGCGCAGGTGCCCCGCT 1207
|||||
Db 1141 GACCATCTTCTGTGGGTTCAGAGGCCCTGAGTGCAGGGACTCCCGCGCAGGTGCCCCGCT 1200
QY 1208 GCGCCAGCGCTACTGGCAATGCGGCCCTGTCTGTGAGCTGCTTGGGAACCAAGCGCA 1267
|||||
Db 1201 GCGCCAGCGCTACTGGCAATGCGGCCCTGTCTGTGAGCTGCTTGGGAACCAAGCGCA 1260
QY 1268 GTGCCCTTACGGGGGTCTCTCAAGACGCACTGCCGCTGCGAGCTCGCGTCAACCCAGC 1327
|||||
Db 1261 GTGCCCTTACGGGGGTCTCTCAAGACGCACTGCCGCTGCGAGCTCGCGTCAACCCAGC 1320
QY 1328 AGCGGTGTGTGTGCCCCGGGAGAGGCCAGGGCTCTGTGGCGGGCCCCGAGGAGGAGA 1387
|||||
Db 1321 AGCGGTGTGTGTGCCCCGGGAGAGGCCAGGGCTCTGTGGCGGGCCCCGAGGAGGAGA 1380
QY 1388 CACAGACCCCGCTGCGCTGTGCAAGTGTCCGCCAGCACAGAGCCCTGGCAGGTGA 1447
|||||
Db 1381 CACAGACCCCGCTGCGCTGTGCAAGTGTCCGCCAGCACAGAGCCCTGGCAGGTGA 1440
QY 1448 CGGCTTGTGGGGGCTGCGCTGCGCGCGCTGTGTGCCCCAGGCGCTTGGGGCTCCAGGCA 1507
|||||
Db 1441 CGGCTTGTGGGGGCTGCGCTGCGCGCGCTGTGTGCCCCAGGCGCTTGGGGGCTCCAGGCA 1500
QY 1508 CAACGAACGCGCTTCTCTAGGAACACCAAGATTATCTCCCTGGGGAAGCATGCCAA 1567
|||||
Db 1501 CAACGAACGCGCTTCTCTAGGAACACCAAGATTATCTCCCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCTGAGGAGCTGACGTGAAGATGAGCGTGCAGGACTGCGCTTGGCTGCGCAG 1627
|||||
Db 1561 GCTCTGCTGAGGAGCTGACGTGAAGATGAGCGTGCAGGACTGCGCTTGGCTGCGCAG 1620
QY 1628 GAGCCCAAGGGGTGGCTGTGTCTCCGGCCGACAGACCGTCTGCGTGAAGAGATCCTGGC 1687

Db 1621 GAGCCCAAGGGGTGGCTGTGTCTCCGGCCGACAGACACCGTCTGGGTGAGAGATCCTGGC 1680
QY 1688 CAAGTCTCTGACATGGCTGATGATGTGTACGTCTGTCAGAGCTGCTCAGGTCTTCTTTTA 1747
|||||
Db 1681 CAAGTCTCTGACATGGCTGATGATGTGTACGTCTGTCAGAGCTGCTCAGGTCTTCTTTTA 1740
QY 1748 TGTACGAGAGACCACTTCAAAAAGACAGGCTCTTTTCTTACCGGAAGAGTGTCTGAG 1807
|||||
Db 1741 TGTACGAGAGACCACTTCAAAAAGACAGGCTCTTTTCTTACCGGAAGAGTGTCTGAG 1800
QY 1808 CAAGTTCAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTGTC 1867
|||||
Db 1801 CAAGTTCAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1927
|||||
Db 1861 GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1920
QY 1928 CTTATCCCAAGCCTGACGGGCTGCGCGCGATTGTGAACATGSACTACGTCTGGAGC 1987
|||||
Db 1921 CTTATCCCAAGCCTGACGGGCTGCGCGCGATTGTGAACATGSACTACGTCTGGAGC 1980
QY 1988 CAGAAGTTCGCGACAGAAAAAGAGGGCGAGCGTCTACCTCGAGGCTGAAGCACACTGTT 2047
|||||
Db 1981 CAGAAGTTCGCGACAGAAAAAGAGGGCGAGCGTCTACCTCGAGGCTGAAGCACACTGTT 2040
QY 2048 CAGCGTGTCAACTACGAGCGGGCGCGCGCGCGCGCTCTCTGGCGCTCTGTGCTGGG 2107
|||||
Db 2041 CAGCGTGTCAACTACGAGCGGGCGCGCGCGCGCGCGCTCTCTGGCGCTCTGTGCTGGG 2100
QY 2108 CCTGACGATATCCACAGAGGGCTGGCGCACCTTCTGCTGCTGTGTGCGGGGCCAGGACCC 2167
|||||
Db 2101 CCTGACGATATCCACAGAGGGCTGGCGCACCTTCTGCTGCTGTGTGCGGGGCCAGGACCC 2160
QY 2168 GCGCGCTGAGCTGTA-----CATCCCCCA 2191
|||||
Db 2161 GCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGGCGCGTACGACACCATCCCCCA 2220
QY 2192 GGACAGGCTCAAGGAGTATCGCCAGCATCATCAAAACCCAGAACAGCTACTGCTGCG 2251
|||||
Db 2221 GGACAGGCTCAAGGAGTATCGCCAGCATCATCAAAACCCAGAACAGCTACTGCTGCG 2280
QY 2252 TCGTATGCGCGTGTCCAGAAAGCGCCCATGGGCAGCTCCGCAAGCGCTTCAAGAGCCA 2311
|||||
Db 2281 TCGTATGCGCGTGTCCAGAAAGCGCCCATGGGCAGCTCCGCAAGCGCTTCAAGAGCCA 2340
QY 2312 CGTCTTACTTGAACAGACCTCCAGCGCTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2371
|||||
Db 2341 CGTCTTACTTGAACAGACCTCCAGCGCTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400
QY 2372 GACCAGCCCGCTGAGGGATGCCGTGTCATCGACAGAGCTCTCTCTGAATGAGGCCAG 2431
|||||
Db 2401 GACCAGCCCGCTGAGGGATGCCGTGTCATCGACAGAGCTCTCTCTGAATGAGGCCAG 2460
QY 2432 CAGTGGCGCTTTCGACGCTTCTTACGCTTATGTGCCACACAGCGCGTGCATCAGGGG 2491
|||||
Db 2461 CAGTGGCGCTTTCGACGCTTCTTACGCTTATGTGCCACACAGCGCGTGCATCAGGGG 2520
QY 2492 CAAGTCTTACGTCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGTG 2551
|||||
Db 2521 CAAGTCTTACGTCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGTG 2580
QY 2552 CAGCGTGTGCTACGGCGACATGAGAAACAGCTGTTTGCGGGGATTCGCGGGAGCGGCT 2611
|||||
Db 2581 CAGCGTGTGCTACGGCGACATGAGAAACAGCTGTTTGCGGGGATTCGCGGGAGCGGCT 2640
QY 2612 GCTCTGCGTTGGTGGATGATTTCTTGTGTGTGACACCTCACCTTCACCGCGAAAC 2671
|||||
Db 2641 GCTCTGCGTTGGTGGATGATTTCTTGTGTGTGACACCTCACCTTCACCGCGAAAC 2700
QY 2672 CTTCTTACGAGCCCTGTGTCGAGGTGTCCTGAGTATGCGTGCCTGTGAACCTTGCAGAA 2731
|||||

Db 2701 CTTCTCAGAGACCTGGTCCGAGGTTGCCCTGAGTATGCGCTGCGTGTGAACCTTGGCGAA 2760
QY 2732 GACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTTGTTCAGAT 2791
Db 2761 GACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTTGTTCAGAT 2820
QY 2792 GCGGGCCACGGGCTATTCCTCGTGGTGGCGCTGCTGTGGATACCGGGACCCCTGGAGGT 2851
Db 2821 GCGGGCCACGGGCTATTCCTCGTGGTGGCGCTGCTGTGGATACCGGGACCCCTGGAGGT 2880
QY 2852 GCAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG 2911
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGAGAGACATGCGTGGCAACTCTTTGGGGTCTTGGCGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGAGAGACATGCGTGGCAACTCTTTGGGGTCTTGGCGCTGAAGTG 3000
QY 2972 TCACAGCCGTGTTCTGGATTGTCAGAGTGAACAGCCCTCCAGAGCGGTGTGCACCAACATCTA 3031
Db 3001 TCACAGCCGTGTTCTGGATTGTCAGAGTGAACAGCCCTCCAGAGCGGTGTGCACCAACATCTA 3060
QY 3032 CAAGATCCTCCTGCTGCAGCGGTACAGGTTTTCACGATGTGTGCTGCAGCTCCCATTTTCA 3091
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QY 3332 GCTGAGTCGGAAGCTCCCGGGAGACGAGCTGACTGCCCTGGAGGGCCGCAACCCGGC 3391
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XX
DT 06-OCT-1999 (first entry)
XX
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KW Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
KW body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
KW acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
KW breast cancer; ss.
XX
OS Homo sapiens.
XX
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XX
PD 05-AUG-1999.
XX
PF 04-FEB-1998; 98DE-1004372.
XX
PR 04-FEB-1998; 98DE-1004372.
XX
PA (DAHM/) DAHM M W.
XX
PI Dahm MW;
XX
DR WPI; 1999-431408/37.
XX
PT Quantifying tumor cells by amplifying mRNA encoding the catalytic
PT subunit of telomerase
XX
PS Example; Fig 1A-B; 26pp; German.
XX
CC This invention describes a novel method for the quantitation of tumour
CC cells in a body fluid which comprises (1) enrichment or isolation of
CC tumour cells in the sample, (2) amplification of mRNA from these cells
CC that encodes the catalytic subunit of telomerase and (3) quantifying
CC the amount of amplified mRNA. The method is applied to tumour cells
CC derived from (micro)metastases, e.g. associated with a wide range of
CC tumours such as T-cell lymphoblastoma, chronic myeloid or acute
CC lymphatic leukemia, melanoma, pulmonary carcinoma, cancer of colon or
CC breast etc. This sequence encodes a human telomerase protein catalytic
CC domain.
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;
Query Match 99.1%; Score 3969; DB 20; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-147;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
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Db 127

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QY 128 GCCGCTGGCCACGTTGCTGCGGGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGAGCGCGG 187
Db 121 GCCGCTGGCCACGTTGCTGCGGGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGAGCGCGG 180
QY 188 GGACCCGGGGCTTTCGCGCGCGCTGGTGGGCCAGTGCCTGGTGTGCGTGGCCCTGGGACGC 247
Db 181 GGACCCGGGGCTTTCGCGCGCGCTGGTGGGCCAGTGCCTGGTGTGCGTGGCCCTGGGACGC 240
QY 248 ACGGCGGG 307
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QY 308 CCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGGAGAACGTGCTGGCCTTCGGCTTCGC 367
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Db 601 TCAGGGCGGG 660
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Db 961 GCACACAGCGGG 1020
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QY 1448 GCGCTTGTGCGGG 1507
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QY	2372	GACCAAGCCCGCTGAGGGATGCCGTGTCATGACAGACAGCTCCTCCGTAATGAGGCCAG	2431
Db	2401	GACCAAGCCCGCTGAGGGATGCCGTGTCATGACAGACAGCTCCTCCGTAATGAGGCCAG	2460
QY	2432	CAGTGGCCCTTGCAGCGTCTTCCTACGCTTCATGTGCCAACCGCCGTGGCATTCAGGG	2491
Db	2461	CAGTGGCCCTTGCAGCGTCTTCCTACGCTTCATGTGCCAACCGCCGTGGCATTCAGGG	2520
QY	2492	CAAGTCTTACGTCAGTGCCAGTGGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTCG	2551
Db	2521	CAAGTCTTACGTCAGTGCCAGTGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTCG	2580
QY	2552	CAGCCTGTGCTACGGCGGACATGGAAGACAAGCTGTTTGGGGGATTCGGCGGACGGGCT	2611
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QY	2732	GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTGTTCCAGAT	2791
Db	2761	GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTGTTCCAGAT	2820
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QY	3032	CAAGATCTCTCTGCTGACAGGCGCTACAGGTTTCACGCACTGTGTGCTGACGCTCCATTTC	3091
Db	3061	CAAGATCTCTCTGCTGACAGGCGCTACAGGTTTCACGCACTGTGTGCTGACGCTCCATTTC	3120
QY	3092	TCAGCAGGTTTGAGAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGCTCCCT	3151
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Q	y	3512	CACACCCAGGCCCGCACCCGCTGGGAGTCTGAGGCCCTGAGTAGTGTTTGGCCGAGGCCCTG		3571
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Q	y	3572	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGATGAGGCTTGAGCGAGTGTCCAGCCAAAGGCT		3631
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Q	y	3632	GAGTGTCCAGCACACCTGCGCTCTTCACCTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA		3691
D	b	3661	GAGTGTCCAGCACACCTGCGCTCTTCACCTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA		3720
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D	b	3781	CCAGATTCGCCCATTTGTTCAACCCCTCGCCCTGCCCTCCTTTGGCCTTCCACCCCAACCATCC		3840
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D	b	3901	CCCTGTACACAGGCGAAGGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAAATTGGGGG		3960
Q	y	3932	GAGGTGCTGTGGGAGTAATAATACTGATATATGAGTTTTCAGTTTGAAAAAA		3986
D	b	3961	GAGGTGCTGTGGGAGTAATAATACTGATATATGAGTTTTCAGTTTGAAAAAA		4015
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XX	AAH45901;				
XX	06-SEP-2001	(first. entry)			
XX	Human hTERT gene.				
DE					
XX	Human; hTERT; telomerase; catalytic subunit; mRNA quantitation; detection; beta-region; diagnosis; cancer; ds.				
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KW	Human sapiens.				
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XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX      Chang SP, Santini CD;
XX
XX      WPI; 2001-376930/40.
DR

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XX      Quantitating expression of mRNA encoding hTERT, the catalytic subunit
PT      of telomerase, as an indicator of cancer, by amplifying RNA using
PT      primers complementary to hTERT gene sequence and quantitating amplified
PT      products
XX
XX      Claim 1; Page 5-7; 29pp; English.
PS
XX
XX      The present sequence is that of the hTERT gene encoding the catalytic
CC      subunit of the human telomerase, comprising 16 exons, which is useful in
CC      a method for quantitating hTERT mRNA. The method is useful for detecting
CC      the presence of beta-region (a 182 nucleotide region consisting of exons
CC      7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis
CC      of cancer. The method provides an accurate measure of telomerase activity
CC      by selectively measuring mRNA that encodes an active hTERT protein.
XX
SQ      Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;
Query Match          99.1%; Score 3969; DB 22; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-147;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY      8 GCAGCGCTGCTCTGTCGCGACAGTGGAGAGCCCTGGCCCCGGCCACCCCGCATGCC 67
Db      1 GCAGCGCTGCTCTGTCGCGACAGTGGAGAGCCCTGGCCCCGGCCACCCCGCATGCC 60
QY      68 GCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGACACCTACCGCGAGTGTCT 127
Db      61 GCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGACACCTACCGCGAGTGTCT 120
QY      128 GCGCGCTGCGACAGTGTGCGCGCGCTGCGCGCCAGCGGCTGGCGCTGTGACGCGCG 187
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QY      188 GGAACCCGGCGGCTTCCCGCGCGCTGTGCGCCAGTGTGCTGTGCGTCCCTGGGACGC 247
Db      181 GGAACCCGGCGGCTTCCCGCGCGCTGTGCGCCAGTGTGCTGTGCGTCCCTGGGACGC 240
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Db      481 CCGCGTGGCGCGAGCGTGTGCTTCACTGCTGCGACGCTGCGCGCTTTCGTGTGCT 540
QY      548 GCGTCCAGCTGCGCGCTTACAGGTGTGCGCGCGCGCGCGCTGTACAGCTGCGCGCTGCCAC 607
Db      541 GCGTCCAGCTGCGCGCTTACAGGTGTGCGCGCGCGCGCGCTGTACAGCTGCGCGCTGCCAC 600
QY      608 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
Db      601 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY      668 CTGAACCATAGCGTACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 727
Db      661 CTGAACCATAGCGTACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 720
QY      728 GAGCGCGCGCGCGCGAGTGTGCGCGCGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCG 787
Db      721 GAGCGCGCGCGCGCGAGTGTGCGCGCGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCG 780

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Db 2941 CGGCTTCAAGGCTGGAGGAACATGCGCAAACTCTTTGGGCTTGGCGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGATTTGACAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3031
Db 3001 TCACAGCCTGTTTCTGATTTGACAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060
QY 3032 CAAGATCCCTCTGCTGCAGGCGGTACAGTTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3091
Db 3061 CAAGATCCCTCTGCTGCAGGCGGTACAGTTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
QY 3092 TCAGCAAGTTTGAAGAACCACCATTTTCTGCGGCTCATCTGTGACACAGGCGCTCCCT 3151
Db 3121 TCAGCAAGTTTGAAGAACCACCATTTTCTGCGGCTCATCTGTGACACAGGCGCTCCCT 3180
QY 3152 CTGCTACTTCATCTCTGAAGCCCAAGACGAGGATGTGCTGGGGCCAAAGGGCGCGC 3211
Db 3181 CTGCTACTTCATCTCTGAAGCCCAAGACGAGGATGTGCTGGGGCCAAAGGGCGCGC 3240
QY 3212 CGGCCCTGCTCCCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCAATTCCTGCTCAAGCT 3271
Db 3241 CGGCCCTGCTCCCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCAATTCCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGTGTACCTACGTGCACTCTCTGGGGTCACTCAGACAGCCCAAGCGCA 3331
Db 3301 GACTCGACACCGTGTACCTACGTGCACTCTCTGGGGTCACTCAGACAGCCCAAGCGCA 3360
QY 3332 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCCCTGGAGCGCCAGCCAAACCGGC 3391
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCCCTGGAGCGCCAGCCAAACCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTCTGAGCTGATGGCCACCCGCCCAAGCCAGCGCGA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTCTGAGCTGATGGCCACCCGCCCAAGCCAGCGCGA 3480
QY 3452 GAGCAGACACGACGAGCCCTGTACAGCGGGGCTTACGTCCAGGAGGAGGGGGCGGC 3511
Db 3481 GAGCAGACACGACGAGCCCTGTACAGCGGGGCTTACGTCCAGGAGGAGGGGGCGGC 3540
QY 3512 CACACCCAGGCGCGCACCGCTGGAGTCTGAGGCGCTGAGTGTGTTGGCGGAGGCGCTG 3571
Db 3541 CACACCCAGGCGCGCACCGCTGGAGTCTGAGGCGCTGAGTGTGTTGGCGGAGGCGCTG 3600
QY 3572 CATGTCCGCTGAAGGCTGAGTGTCCGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT 3631
Db 3601 CATGTCCGCTGAAGGCTGAGTGTCCGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGCTTTCACCTTCCACACAGGCTGGCGCTCGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGCTTTCACCTTCCACACAGGCTGGCGCTCGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCTCCTACACAGAGAGCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTTCTCCTACACAGAGAGCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTCGCCATTGTTCACCCCTGCGCTGCCCTCTCTTGGCTTCCACCCCAACCATCC 3811
Db 3781 CCAGATTCGCCATTGTTCACCCCTGCGCTGCCCTCTCTTGGCTTCCACCCCAACCATCC 3840
QY 3812 AGGTGAGACCTTGAGAGGACCTGAGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3871
Db 3841 AGGTGAGACCTTGAGAGGACCTGAGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGGCGAGGACCTGCACTGATGGGGTCCCTGTGGGTCAAAATTGGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCTGCACTGATGGGGTCCCTGTGGGTCAAAATTGGGGG 3960
QY 3932 GAGGTGCTGTGGGAGTAATAATACTGATATATAGAGTTTTCAGTTTGAAAAAA 3986
Db 3961 GAGGTGCTGTGGGAGTAATAATACTGATATATAGAGTTTTCAGTTTGAAAAAA 4015

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ABA97534
ID ABA97534 standard; DNA; 4015 BP.
XX
AC ABA97534;
XX
DT 05-APR-2002 (first entry)
XX
DE Cancer cell discrimination method related human DNA.
XX
KW Human; telomerase; enzyme; cancer cell discrimination; gene;
KW reverse transcriptase; ds.
XX
OS Homo sapiens.
XX
PN JP2001309791-A.
XX
PD 06-NOV-2001.
XX
PF 02-MAY-2000; 2000JP-0138250.
XX
PR 02-MAY-2000; 2000JP-0138250.
XX
PA (KANE/) KANEUCHI H.
PA (KAMI/) KAMIMORI M.
XX
DR WPI; 2002-134853/18.
XX
PT Discrimination of a cancer cell in a sample tissue, comprises
PT determining the expression level of a reverse transcriptase component
PT of telomerase using a hybridization assay -
XX
PS Claim 2; Page 9-10; 16pp; Japanese.
XX
CC The present invention relates to a method for the discrimination of a
CC cancer cell in a sample tissue, which involves determining the expression
CC level of a reverse transcriptase component of telomerase in a cell
CC constituting the sample tissue by an in situ hybridization of the mRNA of
CC the enzyme, and judging a cell showing a higher expression level than
CC that of the reverse transcriptase component of telomerase in a normal
CC cell to be a cancer cell. The present sequence is a human DNA used in the
CC exemplification of the invention.
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 other;

Query Match 99.1%; Score 3969; DB 24; Length 4015;
Best Local Similarity 99.1%; Pred. No. 9.4e-147;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCCCGGCACCCCGGATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCCCGGCACCCCGGATGCC 60
QY 68 GCGCGTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGACGCACTACCGAGGTGCT 127
Db 61 GCGCGTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGACGCACTACCGAGGTGCT 120
QY 128 GCGGCTGGCAAGTTGCTGCGGCGCGTGGGGCCCCAGGGCTGGCGGTGTCAGCGGG 187
Db 121 GCGGCTGGCAAGTTGCTGCGGCGCGTGGGGCCCCAGGGCTGGCGGTGTCAGCGGG 180
QY 188 GGACCCGGCGGCTTTCGCGCGCTGTGCGCCAGTGCCTGTGCTGCCCTGGAGCG 247
Db 181 GGACCCGGCGGCTTTCGCGCGCTGTGCGCCAGTGCCTGTGCTGCCCTGGAGCG 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCTTCCGCCAGGTGTCTGCTGAAGAGCTGTGGC 307
Db 241 ACGGCGCGCGCGCGCGCGCGCGCTTCCGCCAGGTGTCTGCTGAAGAGCTGTGGC 300
QY 308 CCGAGTGTGAGAGGCTGTGAGAGCGCGCGGAGGAAGCTGCTGGCTTGGCTTGC 367
Db 301 CCGAGTGTGAGAGGCTGTGAGAGCGCGCGGAGGAAGCTGCTGGCTTGGCTTGC 360
QY 368 GCTGCTGAGCGGGGCGCGCGGGGCGCGCGCGCGGAGGCTTACACACAGCGTGGCAGCTA 427

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Db	361	GCTGTGACGGGGCCCGGGGGCCCCCGAGGCGTTCAACACAGCGTGGCCAGCTA	420
QY	428	CTTGCCCAACACGGGTGACCGGACGCACTGCGGGGGAGCGGGGGCGTGGGGCGTGTGCTGCG	487
Db	421	CCTGCCCAACACGGGTGACCGGACGCACTGCGGGGGAGCGGGGGCGTGGGGCGTGTGCTGCG	480
QY	488	CCGGGTGGGGGACGACGCTGCTGTCTACCTCTGGACAGCTGCGGCTCTTTGTGCTGCT	547
Db	481	CCGGGTGGGGGACGACGCTGCTGTCTACCTCTGGACAGCTGCGGCTCTTTGTGCTGCT	540
QY	548	GGCTCCCAAGCTGCGGCTTACAGGTGTGCGGGCGCGCGCTGTACCAAGCTCGGGCGTGGCCAC	607
Db	541	GGCTCCCAAGCTGCGGCTTACAGGTGTGCGGGCGCGCGCTGTACCAAGCTCGGGCGTGGCCAC	600
QY	608	TCAGGCGCGGGCCCCCGCCACACGCTTAGTGACCCCCGAAGGGCGTCTGGGATGCGAACGGGC	667
Db	601	TCAGGCGCGGGCCCCCGCCACACGCTTAGTGACCCCCGAAGGGCGTCTGGGATGCGAACGGGC	660
QY	668	CTGAACCATAGCGTACAGGAGCGGGGGTCCCCCTGGGCGTGCACGCCCGGCTGCGAG	727
Db	661	CTGAACCATAGCGTACAGGAGCGGGGGTCCCCCTGGGCGTGCACGCCCGGCTGCGAG	720
QY	728	GAGGCGGGGGGACATGTCACAGCCGAAGTCTGCCGTGTGCCCAAGAGGCCACAGCGTGGCGC	787
Db	721	GAGGCGGGGGGACATGTCACAGCCGAAGTCTGCCGTGTGCCCAAGAGGCCACAGCGTGGCGC	780
QY	788	TGCCCCGTGAGCCCGAGCGAGCGCCGTTGGGCAAGGGTCTTGCGGCCACCCGGGACAGGAC	847
Db	781	TGCCCCGTGAGCCCGAGCGAGCGCCGTTGGGCAAGGGTCTTGCGGCCACCCGGGACAGGAC	840
QY	848	GCGTGGACCGAGTACCGTGGTCTGTGTGTGTGTCTACCTGCCACAGACCCGCCGAGAAGAC	907
Db	841	GCGTGGACCGAGTACCGTGGTCTGTGTGTGTGTCTACCTGCCACAGACCCGCCGAGAAGAC	900
QY	908	CACCTCTTTGGAGGGTGGCTCTCTGGACGCGGCCACCTCCCAATCCCTGGGGCCGCCA	967
Db	901	CACCTCTTTGGAGGGTGGCTCTCTGGACGCGGCCACCTCCCAATCCCTGGGGCCGCCA	960
QY	968	GCACCAAGCGGGCCCCCATTCACATCGCGGGCCACACAGTCCCTGGGACACGCGTTGTCC	1027
Db	961	GCACCAAGCGGGCCCCCATTCACATCGCGGGCCACACAGTCCCTGGGACACGCGTTGTCC	1020
QY	1028	CCCGGTGTACGCCGAGACCAAGACTTCTCTACTCTCCTACAGCGCAAGAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACGCCGAGACCAAGACTTCTCTACTCTCCTACAGCGCAAGAGAGCAGCTGCG	1080
QY	1088	GCCCTCTCTCTACTACGCTCTGTGAGGCCACGCTGAGCTGGCGCTCGAGGCTCTGTGA	1147
Db	1081	GCCCTCTCTCTACTACGCTCTGTGAGGCCACGCTGAGCTGGCGCTCGAGGCTCTGTGA	1140
QY	1148	GACCATCTTTCTGGGTTCCAGGCGCTTGATGCCAAGGACTCCCCGAGGTTGCCCGGCT	1207
Db	1141	GACCATCTTTCTGGGTTCCAGGCGCTTGATGCCAAGGACTCCCCGAGGTTGCCCGGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAAAATGCGGCCCTCTTCTGTGAGCTGTGGGAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAAATGCGGCCCTCTTCTGTGAGCTGTGGGAACCAAGCGCA	1260
QY	1268	GTGCCCTTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGTGCGGTACACCCAGC	1327
Db	1261	GTGCCCTTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGTGCGGTACACCCAGC	1320
QY	1328	AGCCGCTCTGTGCGCGGAGAGACCCCAAGGGCTCTGTGGCGGGCCCCGAGAGGAGGA	1387
Db	1321	AGCCGCTCTGTGCGCGGAGAGACCCCAAGGGCTCTGTGGCGGGCCCCGAGAGGAGGA	1380
QY	1388	CACAGACCCCGTGGCTGTGTGAGCTGTCTCCGCAAGCAGCAAGACGCCCTGTGGAGGTGA	1447
Db	1381	CACAGACCCCGTGGCTGTGTGAGCTGTCTCCGCAAGCAGCAAGACGCCCTGTGGAGGTGA	1440
QY	1448	CGGCTTGGTGGGGCGCTGCGCGCGGCTGTGCCCCAGGCGCTGTGGGGCTCCAGGCA	1507

Db	1441	CGGCTTCGTGCGGGGCGCTGGCCGGCGGTGGTGGCGGCCCGGCCCCCAGAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACCCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGGCCAA	1567
Db	1501	CAACGAACCCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGGCCAA	1560
QY	1568	GCTCTCGCTGCAGAGAGCTGACGTGGGAAGATGACGCTGGCGGACTGGCCTTGGCTGCAG	1627
Db	1561	GCTCTCGCTGCAGAGAGCTGACGTGGGAAGATGACGCTGGCGGACTGGCCTTGGCTGCAG	1620
QY	1628	GAGCCCAAGGGGTGGCGTGTGTTCGGCGCCGACAGACACCCTCTGCGTGAAGAGATCTGGC	1687
Db	1621	GAGCCCAAGGGGTGGCGTGTGTTCGGCGCCGACAGACACCCTCTGCGTGAAGAGATCTGGC	1680
QY	1688	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCACGAGAGACCAACGTTTCAAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCACGAGAGACCAACGTTTCAAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGCGGAGCTGTC	1867
Db	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGCAGCATCGGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCTGACAGGGGCTGGCGCCGATTTGTGAACATGGACTACGTGCTGGAGC	1987
Db	1921	CTTCATCCCCCAAGCTGACAGGGGCTGGCGCCGATTTGTGAACATGGACTACGTGCTGGAGC	1980
QY	1988	CAGAACGTTCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGTCACTACGACAGCGGGCGCGCCCGCGCTCTGGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCACTACGACAGCGGGCGCGCCCGCGCTCTGGCGCTCTGTGCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCCTGGCGCACTTCTGTGCTGCTGTGGCGGCCACAGAACCC	2167
Db	2101	CCTGACGATATCCACAGGGCCTGGCGCACTTCTGTGCTGCTGTGGCGGCCACAGAACCC	2160
QY	2168	GCCGCCTGAGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCCTGAGCTGTA-----CATCCCCCA	2220
QY	2192	GGACAGGCTCACGGAGGTGATGCCAGCATCATCAAAACCAGAAACACGTACTGGCGG	2251
Db	2221	GGACAGGCTCACGGAGGTGATGCCAGCATCATCAAAACCAGAAACACGTACTGGCGG	2280
QY	2252	TGCGTATGCGTGGTTCAGAAAGCCGCCCATGGGGCACGTCCGCAAGGCTTCAAGAGCCA	2311
Db	2281	TGCGTATGCGTGGTTCAGAAAGCCGCCCATGGGGCACGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2312	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTCAGGA	2371
Db	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTCAGGA	2400
QY	2372	GACCAGCCCGCTGAGGGATGCCGTGTCATGAGCAGAGCTCCTCCGTGAATGAGGCCAG	2431
Db	2401	GACCAGCCCGCTGAGGGATGCCGTGTCATGAGCAGAGCTCCTCCGTGAATGAGGCCAG	2460
QY	2432	CAGTGGCTCTTCGAGCTCTTCTCTACGCTTCATGTGTCACACCAAGCCGTCGCGCATAGGGG	2491
Db	2461	CAGTGGCTCTTCGAGCTCTTCTCTACGCTTCATGTGTCACACCAAGCCGTCGCGCATAGGGG	2520
QY	2492	CAAGTCCCTACGTCACAGTCCAGGGGATCCCGAAGGCTCCATCCTTCCACGCTGCTCTG	2551
Db	2521	CAAGTCCCTACGTCACAGTCCAGGGGATCCCGAAGGCTCCATCCTTCCACGCTGCTCTG	2580

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QY 2552 CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCGGGGGAGCGGGCT 2611
    |||
Db 2581 CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCGGGGGAGCGGGCT 2640
QY 2612 GCTCCTGCGTTTGGTGGATGATTTCTTGTGGTACACCTCACCTCACCCACGCGAAAC 2671
    |||
Db 2641 GCTCCTGCGTTTGGTGGATGATTTCTTGTGGTACACCTCACCTCACCCACGCGAAAC 2700
QY 2672 CTTCTCAGAGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAAGTTCGGAA 2731
    |||
Db 2701 CTTCTCAGAGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAAGTTCGGAA 2760
QY 2732 GACAGTGTGAAGTTCCTCTAGAGACGAGGCGCTGGGTGGACAGGCTTTTGTTCAGAT 2791
    |||
Db 2761 GACAGTGTGAAGTTCCTCTAGAGACGAGGCGCTGGGTGGACAGGCTTTTGTTCAGAT 2820
QY 2792 GCGGGCCACGGCCTATTCCTGCTGGTGGCGCTGCTGCTGATACCGGACCTGAGGT 2851
    |||
Db 2821 GCGGGCCACGGCCTATTCCTGCTGGTGGCGCTGCTGCTGATACCGGACCTGAGGT 2880
QY 2852 GCAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACTTCAACCG 2911
    |||
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGGAGGAGAACATGCTGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG 2971
    |||
Db 2941 CGGCTTCAAGGCTGGGAGGAGAACATGCTGCAAACTCTTTGGGGTCTTGGCGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGGATTTGACAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3031
    |||
Db 3001 TCACAGCCTGTTTCTGGATTTGACAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA 3060
QY 3032 CAAGATCCTCCTGCTGTCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3091
    |||
Db 3061 CAAGATCCTCCTGCTGTCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120
QY 3092 TCAGCAAGTTTGGAGAAGAACCCACATTTTCTGCGGTCATCTGTGACAGGCGCTCCCT 3151
    |||
Db 3121 TCAGCAAGTTTGGAGAAGAACCCACATTTTCTGCGGTCATCTGTGACAGGCGCTCCCT 3180
QY 3152 CTGCTACTTCATCTCTGAAGCCCAAGACGAGGGATGTGCTGGGGCCAAAGGGCGCGC 3211
    |||
Db 3181 CTGCTACTTCATCTCTGAAGCCCAAGACGAGGGATGTGCTGGGGCCAAAGGGCGCGC 3240
QY 3212 CGGCCCTTGCCCTCCGAGGCGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271
    |||
Db 3241 CGGCCCTTGCCCTCCGAGGCGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGTGTACACCTACGTGCCACTCTGGGTCACCTCAGACAGCCAGACGCA 3331
    |||
Db 3301 GACTCGACACCGTGTACACCTACGTGCCACTCTGGGTCACCTCAGACAGCCAGACGCA 3360
QY 3332 GCTGAGTCGGAAGCTCCCGGGAGACAGCCTGACTGCCCTGGAGCGCCAGCCAAACCGGC 3391
    |||
Db 3361 GCTGAGTCGGAAGCTCCCGGGAGACAGCCTGACTGCCCTGGAGCGCCAGCCAAACCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGGAAGTGTGAGGCTGAGGCGCCAGAGCGCGGA 3451
    |||
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGGAAGTGTGAGGCTGAGGCGCCAGAGCGCGGA 3480
QY 3452 GAGCAGACACCGAGCAGCCCTGTACAGCGCGGCTCTACGTCCAGAGGAGGAGGCGCGCC 3511
    |||
Db 3481 GAGCAGACACCGAGCAGCCCTGTACAGCGCGGCTCTACGTCCAGAGGAGGAGGCGCGCC 3540
QY 3512 CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGAGGCGCGCTG 3571
    |||
Db 3541 CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGAGGCGCGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT 3631
    |||
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT 3660

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QY 3632 GAGTGTCCAGCACACCTGCCGCTCTTCACTTCCCCACAGAGGCTGGCGCTGGGCTCCACCCCA 3691
    |||
Db 3661 GAGTGTCCAGCACACCTGCCGCTCTTCACTTCCCCACAGAGGCTGGCGCTGGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCTCAGCAGGAGCGCGGCTTCCACTCCACATAGAAATGATCATCC 3751
    |||
Db 3721 GGGCCAGCTTTTCTCAGCAGGAGCGCGGCTTCCACTCCACATAGAAATGATCATCC 3780
QY 3752 CCAGATTGCGCATTTTACCCCTCGCCCTGCCCTCTTGGCTTCCACCCACCATCC 3811
    |||
Db 3781 CCAGATTGCGCATTTTACCCCTCGCCCTGCCCTCTTGGCTTCCACCCACCATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAGAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3871
    |||
Db 3841 AGGTGAGACCCCTGAGAAGAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGCTCAAAATTGGGGG 3931
    |||
Db 3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGCTCAAAATTGGGGG 3960
QY 3932 GAGTGTCTGGGAGTAAATACTGAATATGAGTTTTCAGTTTGAAGAAAAA 3986
    |||
Db 3961 GAGTGTCTGGGAGTAAATACTGAATATGAGTTTTCAGTTTGAAGAAAAA 4015

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RESULT 10
AAZ08150
ID AAZ08150 standard; cDNA; 4015 BP.

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XX
AC AAZ08150;

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DT 17-JAN-2000 (first entry)

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XX
DE Human telomerase reverse transcriptase cDNA.

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KW Human telomerase reverse transcriptase; hTERT; telomerase; hEST2;
KW catalytic protein component; cell proliferative capacity;
KW cell immortality; neoplastic phenotype; diagnostic application;
KW prognostic application; telomerase related condition; cancer;
KW therapeutic agent; telomerase expression; telomerase activity; ds.

```

```

XX
OS Homo sapiens.

```

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FH Key Location/Qualifiers
FT CDS 56..3454

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FT /tag= a
FT /product= "Human telomerase reverse transcriptase"
FT /transl_except= (pos:1877..1879, aa:Gln)

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PN WO950279-A1.

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PD 07-OCT-1999.

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PF 31-MAR-1999; 99WO-US07160.

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PR 31-MAR-1998; 98US-0052919.

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PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.

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PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;

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DR WPI; 1999-610834/52.

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DR P-PSDB; AAY28881.

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XX Antisense polynucleotides for human telomerase reverse transcriptase
XX used for diagnosing or treating cancer.

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PS Claim 1; Fig 1; 31pp; English.

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XX The present sequence encodes for human telomerase reverse transcriptase
XX (hTERT). This is the catalytic protein component of telomerase and is also
CC

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CC referred to as hEST2. This correlates with cell proliferative capacity,
CC cell immortality, and the development of a neoplastic phenotype. Human
CC TRT antisense oligonucleotides are useful for diagnostic or prognostic
CC applications to telomerase related conditions, including cancer. They are
CC also useful as therapeutic agents, for inhibition of telomerase
expression and activity.

XX
SQ Sequence 4015 BP; 663 A; 1364 C; 1274 G; 714 T; 0 other;

Query Match 99.0%; Score 3967.4; DB 20; Length 4015;
Best Local Similarity 99.1%; Pred. No. 1.1e-146;
Matches 3978; Conservative 0; Mismatches 1; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGCT 127
Db 61 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGCT 120
QY 128 GCCGCTGGCAGCTTGTGCGGGCGCTGGGGCCCCAGGGCTGGCGCTGTGCACGGCGG 187
Db 121 GCCGCTGGCAGCTTGTGCGGGCGCTGGGGCCCCAGGGCTGGCGCTGTGCACGGCGG 180
QY 188 GGAACCCGGCGGCTTCCGCGCGCTGGTGGCCCCAGTGCCTGCTGTGCTGCCCTGGGAGCG 247
Db 181 GGAACCCGGCGGCTTCCGCGCGCTGGTGGCCCCAGTGCCTGCTGTGCTGCCCTGGGAGCG 240
QY 248 AGGGCCCGCCCCCGCCCCCTCTTCCGCCAGTGTCTCTGCTGAAGAGAGCTGTGGC 307
Db 241 AGGGCCCGCCCCCGCCCCCTCTTCCGCCAGTGTCTCTGCTGAAGAGAGCTGTGGC 300
QY 308 CGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGGAAGACGTGTGCGCTTCCGCTTCCG 367
Db 301 CGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGGAAGACGTGTGCGCTTCCGCTTCCG 360
QY 368 GCTGCTGGACGG 427
Db 361 GCTGCTGGACGG 420
QY 428 CCTGCCCAACACGGGTGACCGCAGCTGCGGGGAGCGGGGGCGTGGGGGGCTGTCTGCG 487
Db 421 CCTGCCCAACACGGGTGACCGCAGCAGCTGCGGGGAGCGGGGGCGTGGGGGGCTGTCTGCG 480
QY 488 CCGCGTGGCGACGAGCTGTGCTTACCTGTGTCAGCGCTGCGCGCTTGTGTCTGTGT 547
Db 481 CCGCGTGGCGACGAGCTGTGCTTACCTGTGTCAGCGCTGCGCGCTTGTGTCTGTGT 540
QY 548 GCGTCCCAAGCTGCGCTTACAGGCTGTGCGGGCGCGCGCTGTACCACTGCGCGCTGCCAC 607
Db 541 GCGTCCCAAGCTGCGCTTACAGGCTGTGCGGGCGCGCGCTGTACCACTGCGCGCTGCCAC 600
QY 608 TCAGGGCCCCGG 667
Db 601 TCAGGGCCCCGG 660
QY 668 CTGGAACCATATAGCTCAGAGGAGCGCGGGGTCCCGCTGGGCTGCGAGCCCGGGTGGAG 727
Db 661 CTGGAACCATATAGCTCAGAGGAGCGCGGGGTCCCGCTGGGCTGCGAGCCCGGGTGGAG 720
QY 728 GAGGGCGGGGGGAGTGCCAGCCGGAATGTGCCGTGGCCCAAGAGGCCCAAGCGGTGGCG 787
Db 721 GAGGGCGGGGGGAGTGCCAGCCGGAATGTGCCGTGGCCCAAGAGGCCCAAGCGGTGGCG 780
QY 788 TGCCCTTGAAGCGGAGCGGAGCGCCGTTGGGAGAGGGGTCTGGGCCCAACCGGCGAGGAC 847
Db 781 TGCCCTTGAAGCGGAGCGGAGCGCCGTTGGGAGAGGGGTCTGGGCCCAACCGGCGAGGAC 840
QY 848 GCGTGAACCGAGTGAACCGTGTCTGTGTGTGTGTCACTGCGACACCGCGCGAAGAGC 907
Db 841 GCGTGAACCGAGTGAACCGTGTCTGTGTGTGTGTCACTGCGACACCGCGCGAAGAGC 900

QY 908 CACCTCTTTGAGAGGTGCGCTCTCTGTGCACGGCCACATCCACCCATCCCTGGGGCCCA 967
Db 901 CACCTCTTTGAGAGGTGCGCTCTCTGTGCACGGCCACATCCACCCATCCCTGGGGCCCA 960
QY 968 GCACCAGCGGG 1027
Db 961 GCACCAGCGGG 1020
QY 1028 CCGGTGTACGGCGAGACCAAGCACTTCTCTACTCTCTCAGCGGACAGAGAGAGCTGGC 1087
Db 1021 CCGGTGTACGGCGAGACCAAGCACTTCTCTACTCTCTCAGCGGACAGAGAGAGCTGGC 1080
QY 1088 GCGCTCTCTCTACTCAGCTCTCTGTAGGGCCAGCCTGACTGGCGCTGGAGAGCTGTGGA 1147
Db 1081 GCGCTCTCTCTACTCAGCTCTCTGTAGGGCCAGCCTGACTGGCGCTGGAGAGCTGTGGA 1140
QY 1148 GACCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGGCT 1207
Db 1141 GACCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGGCT 1200
QY 1208 GCCCAGCGCTACTGGCAAAATGCGGGCCCTGTCTGTGAGCTGTGTGGGAACCAACGCGCA 1267
Db 1201 GCCCAGCGCTACTGGCAAAATGCGGGCCCTGTCTGTGAGCTGTGTGGGAACCAACGCGCA 1260
QY 1268 GTGCCCCCTACGGGGTCTCTCTAAGAGCGACTGCCCGCTCGGAGCTGGGGTCACCCCAGC 1327
Db 1261 GTGCCCCCTACGGGGTCTCTCTAAGAGCGACTGCCCGCTCGGAGCTGGGGTCACCCCAGC 1320
QY 1328 AGCGGTGTCTGTGCTCGGAGAAAGCCCGCAGGGCTGTGTGGCGGGCCCCGAGAGAGAGA 1387
Db 1321 AGCGGTGTGTGTGCTCGGAGAAAGCCCGCAGGGCTGTGTGGCGGGCCCCGAGAGAGAGA 1380
QY 1388 CACAGACCCCGCTGCTGTGTGAGCTGTCTCCGACAGCAGAGAGAGAGAGAGTGA 1447
Db 1381 CACAGACCCCGCTGCTGTGTGAGCTGTCTCCGACAGCAGAGAGAGAGAGAGTGA 1440
QY 1448 CGGCTGTGCGGGGGCTGCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1507
Db 1441 CGGCTGTGCGGGGGCTGCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1500
QY 1508 CAACGAAAGCGCGCTTCTCAGAGAACCAACCAAGATTCAATCTCCCTGGGGAAGCATGCCAA 1567
Db 1501 CAACGAAAGCGCGCTTCTCAGAGAACCAACCAAGATTCAATCTCCCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCTGACAGAGCTGACGTGGAAGATGAGCGTGGCGGAGCTGCGCTTGGCTGGCAG 1627
Db 1561 GCTCTGCTGACAGAGCTGACGTGGAAGATGAGCGTGGCGGAGCTGCGCTTGGCTGGCAG 1620
QY 1628 GAGCCAGGGGTTGGCTGTGTTCGGGGCGGAGACACCGCTGTGCTGAAGAGATCCTGGC 1687
Db 1621 GAGCCAGGGGTTGGCTGTGTTCGGGGCGGAGACACCGCTGTGCTGAAGAGATCCTGGC 1680
QY 1688 CAAGTTCCTGACATGCTGATGATGATGTGTACGTCTGCAAGCTGCTCAAGTCTTTCTTTA 1747
Db 1681 CAAGTTCCTGACATGCTGATGATGATGTGTACGTCTGCAAGCTGCTCAAGTCTTTCTTTA 1740
QY 1748 TGTACGGAGAGACCACTTTCAAAGAAGACAGGCTTTTCTACCGGAAGAGTGTCTGGAG 1807
Db 1741 TGTACGGAGAGACCACTTTCAAAGAAGACAGGCTTTTCTACCGGAAGAGTGTCTGGAG 1800
QY 1808 CAAGTTCGAAAGCATTTGGAATGAGACAGCACTTGAAGAGGTCAGACTGGCGGAGCTGTC 1867
Db 1801 CAAGTTCGAAAGCATTTGGAATGAGACAGCACTTGAAGAGGTCAGACTGGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTGACGAGCATGCGGAAGCCAGGCCCGCTGTGACGTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTGACGAGCATGCGGAAGCCAGGCCCGCTGTGACGTCCAGACTCCG 1920
QY 1928 CTTCATCCCAAGCGCTGACGGGCTGCGGGCGATTGTGAACATGACATCTGCTGGAGAGC 1987
Db 1921 CTTCATCCCAAGCGCTGACGGGCTGCGGGCGATTGTGAACATGACATCTGCTGGAGAGC 1980
QY 1988 CAGACGTTCCGCGAGAAAGAGGGGGCGGAGCGTCTACCTCGAGGGTGAAGGCACTGTT 2047

Db 1981 CAGAACTTCCGAGAGAAAGAGGCGGAGCGTCTACCTCGAGGGTGAAGGCACACTGT 2040
QY 2048 CAGCGTGTCACTACGAGCGGGCGGCGCCCGGCTCTGGGGCTCTGTGTGG 2107
Db 2041 CAGCGTGTCACTACGAGCGGGCGGCGCCCGGCTCTGGGGCTCTGTGTGG 2100
QY 2108 CCTGACGATATCCACAGGCGCTGGCGACCTTCGTGTGGTGTGGGGCCAGAGCC 2167
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QY 2168 GCCGCTGAGTGT-----CATCCCCA 2191
Db 2161 GCCGCTGAGTGTACTTGTCAAGGTGGATGTACGGGCGGCTACGACACCATCCCCA 2220
QY 2192 GGACAGGCTCAGGAGGTATCGCCAGCATCATCAACCCAGAAACAGTACTGTGCG 2251
Db 2221 GGACAGGCTCAGGAGGTATCGCCAGCATCATCAACCCAGAAACAGTACTGTGCG 2280
QY 2252 TCGGTATGCGGTGTCCAGAGGCGCCCATGGGCGACGTCCGCAAGGCTTCAAGAGCA 2311
Db 2281 TCGGTATGCGGTGTCCAGAGGCGCCCATGGGCGACGTCCGCAAGGCTTCAAGAGCA 2340
QY 2312 CGTCTTACCTTGACAGACTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2371
Db 2341 CGTCTTACCTTGACAGACTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400
QY 2372 GACCAGCCCGGTGAGGAGTCCGTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCGAG 2431
Db 2401 GACCAGCCCGGTGAGGAGTCCGTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCGAG 2460
QY 2432 CAGTGGCTCTTCGAGCTTCTTCTACGCTTCATGTGCCACACAGCCGTGGCATCAGGG 2491
Db 2461 CAGTGGCTCTTCGAGCTTCTTCTACGCTTCATGTGCCACACAGCCGTGGCATCAGGG 2520
QY 2492 CAAGTCTTACGTCAGTCCAGTCCAGGGGATCCCGCAGGGCTTCATCTCTCACGCTGCTG 2551
Db 2521 CAAGTCTTACGTCAGTCCAGTCCAGGGGATCCCGCAGGGCTTCATCTCTCACGCTGCTG 2580
QY 2552 CAGCTGTGTACGGCGACATGGAGAACAGCTGTTCGGGGATTCGGCGGAGCGGCT 2611
Db 2581 CAGCTGTGTACGGCGACATGGAGAACAGCTGTTCGGGGATTCGGCGGAGCGGCT 2640
QY 2612 GCTCTGCGTTGTGTGATGATTTCTTGTGTGACACTCACCTCACCCAGCGGAAAC 2671
Db 2641 GCTCTGCGTTGTGTGATGATTTCTTGTGTGACACTCACCTCACCCAGCGGAAAC 2700
QY 2672 CTTCCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGCTGCGTGTGAACCTTGGCGAA 2731
Db 2701 CTTCCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGCTGCGTGTGAACCTTGGCGAA 2760
QY 2732 GACAGTGTGTAACCTCCCTGTAGAAGACGAGGCGCTGGGTGGCACGGCTTTTGTTCAGAT 2791
Db 2761 GACAGTGTGTAACCTCCCTGTAGAAGACGAGGCGCTGGGTGGCACGGCTTTTGTTCAGAT 2820
QY 2792 GCCGGCCACGGCTATTCCTCTGCTGGCGGCTGTGCTGGATACCCGAGCCCTGGAGGT 2851
Db 2821 GCCGGCCACGGCTATTCCTCTGCTGGCGGCTGTGCTGGATACCCGAGCCCTGGAGGT 2880
QY 2852 GCAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG 2911
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGAGGAACATGCGTCCGAACCTTTTGGGGTCTTGGCGGTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGAGGAACATGCGTCCGAACCTTTTGGGGTCTTGGCGGTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGATTTTCAGAGTGAAACAGCTCCAGAGGTGTGACCAACATCTA 3031
Db 3001 TCACAGCCTGTTTCTGATTTTCAGAGTGAAACAGCTCCAGAGGTGTGACCAACATCTA 3060
QY 3032 CAAGATCCTCTGCTGAGGCGGTACAGGTTTCACGCAATGTGTGCTGACGTCCTCAATTCA 3091
|||||

Db 3061 CAAGATCCTCTGCTGACGGGCTACAGGTTTCACCGCATGTGTGCTGACGCTCCCATTTCA 3120
QY 3092 TCACGAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACAGGCGCTCCCT 3151
Db 3121 TCACGAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACAGGCGCTCCCT 3180
QY 3152 CTGCTACTCCATCTGAAAGCCAAAGACGAGGAGTGTGCTGGGGCCAAAGGCGCGC 3211
Db 3181 CTGCTACTCCATCTGAAAGCCAAAGACGAGGAGTGTGCTGGGGCCAAAGGCGCGC 3240
QY 3212 CGGCTCTGCTGCTCCGAGGCGGTGACGTGCTGTGCCAACGATTCCTGTCAAGCT 3271
Db 3241 CGGCTCTGCTGCTCCGAGGCGGTGACGTGCTGTGCCAACGATTCCTGTCAAGCT 3300
QY 3272 GACTCGACACCGTGTACCTACGTGCGCACTCTCTGGGGTCACTCAGACAGCCAGAGCA 3331
Db 3301 GACTCGACACCGTGTACCTACGTGCGCACTCTCTGGGGTCACTCAGACAGCCAGAGCA 3360
QY 3332 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTGAGAGCCGAGCCAGCCGCGC 3391
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTGAGAGCCGAGCCAGCCGCGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTTGACTGATGCGCACCCGCCACAGCCAGCGCA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTTGACTGATGCGCACCCGCCACAGCCAGCGCA 3480
QY 3452 GAGCAGACACGACGACCCCTGTTCACGCGCGGCTCTACGTCACAGGAGGAGGCGGCGC 3511
Db 3481 GAGCAGACACGACGACCCCTGTTCACGCGCGGCTCTACGTCACAGGAGGAGGCGGCGC 3540
QY 3512 CACACCCAGGCGGACCCGCTGGAGTCTGAGGCGCTGAGTGTGGCCAGGCGCTG 3571
Db 3541 CACACCCAGGCGGACCCGCTGGAGTCTGAGGCGCTGAGTGTGGCCAGGCGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGTGTGGCCAGGCGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGTGTGGCCAGGCGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGCTTCTCACTTCCACACAGGCTGCGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGCTTCTCACTTCCACACAGGCTGCGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTCTTCCACACGAGGCGCGGCTTCCACTTCCACATAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTCTTCCACACGAGGCGCGGCTTCCACTTCCACATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTCGCCATTTGTTCAACCCCTGCGCCCTGCGCTTGTGCTTCCACCCCAATCC 3811
Db 3781 CCAGATTCGCCATTTGTTCAACCCCTGCGCCCTGCGCTTGTGCTTCCACCCCAATCC 3840
QY 3812 AGGTGAGAGCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGAGTGACCAAGGTGTG 3871
Db 3841 AGGTGAGAGCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGAGTGACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGTCAAAATTGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGTCAAAATTGGGG 3960
QY 3932 GAGGTGCTGTGGAGTAATAATCTGAATATATAGATTTTCAAGTTTGAAGAAAAA 3986
Db 3961 GAGGTGCTGTGGAGTAATAATCTGAATATATAGATTTTCAAGTTTGAAGAAAAA 4015
RESULT 11
AAx89424
ID AAx89424 standard; cdna; 4027 BP.
XX
AC AAx89424;
XX
DT 22-SEP-1999 (first entry)
XX
DE Human EST2 coding sequence.
XX

KW EST2; proliferative capacity; cellular proliferation; decubitus ulcer;
KW telomerase-activating therapeutic agent; cell life-span extension;
KW venous disease; venous stasis ulcer; excessive pressure; arterial ulcer;
KW tissue regeneration enhancer; atherosclerosis; therapy; ss.
XX Homo sapiens.
XX MO9935243-A2.
XX 15-JUL-1999.
XX 12-JAN-1999; 99WO-US00682.
XX PF 21-APR-1998; 98US-0063657.
XX PR 12-JAN-1998; 98US-0071220.
XX PR 13-JAN-1998; 98US-0071455.
XX (COLD-) COLD SPRING HARBOR LAB.
XX Beach DH, Hannon GJ, Wang J;
XX WPI; 1999-444196/37.
XX DR P-PSDB; AAY28401.
XX
XX Increasing proliferative capacity of cells useful for promoting
XX wound healing
XX
XX Claim 4; Page 65-70; 73pp; English.
XX
XX This sequence encodes the human EST2 protein, and can be used in the
XX method of the invention. The method is for increasing the proliferative
XX capacity of cells, and comprises contacting the cell with a
XX telomerase-activating therapeutic agent (TARA). The method can be used
XX for extending the life-span of cells, e.g. by increasing the number of
XX mitotic divisions. They can be used for e.g. the extension of skin or
XX other epithelial cell cultures or grafts, the expansion of mesenchymal
XX cell cultures or grafts, and the expansion of chondrocyte or osteocyte
XX cultures or grafts. They can be applied to e.g. neuronal, haematopoietic,
XX epithelial, pancreatic, hepatic, chondrocytic and osteocytic stem and
XX progenitor cells in vivo, in vitro or ex vivo protocols. The methods
XX can be used for promoting the healing of wounds resulting from
XX e.g. surgery, burns, inflammation or irritation or ulcers resulting from
XX e.g. venous disease (venous stasis ulcers), excessive pressure (decubitus
XX ulcers) or arterial ulcers. They can also be used to enhance tissue
XX regeneration processes, e.g. of the skin, hair and/or fingernails. They
XX can also be used for treating age-related conditions, e.g. atrophy of the
XX skin through loss of extracellular matrix homeostasis in dermal
XX fibroblasts, age-related macular degeneration caused by accumulation of
XX lipofuscin and downregulation of a neuronal survival factor in retinal
XX pigmented epithelial (RPE) cells, and atherosclerosis caused by loss of
XX proliferative capacity and overexpression of hypertensive and thrombotic
XX factors in endothelial cells. Expanded populations of normal or
XX genetically engineered rejuvenated cells could be used for autologous or
XX allogeneic cell and gene therapy. They can also be used for prolonging
XX the lifespan of a culture of normal cells or tissue being used to secrete
XX therapeutic or other commercially significant proteins and products.
XX
XX Sequence 4027 BP; 674 A; 1361 C; 1277 G; 715 T; 0 other;
QY
Query Match 99.0%; Score 3967; DB 20; Length 4027;
Best Local Similarity 99.0%; Pred. No. 1.1e-146;
Matches 3980; Conservative 0; Mismatches 5; Indels 36; Gaps 1;
QY 13 GCTGCGTCTGTCGCGACAGTGGGAAGCCCTGGCCCCGGGCAACCCCGCGATGCCGCG 72
Db 11 |||||
Db 7 GCGTGTCTCTGTCGCGACAGTGGGAAGCCCTGGCCCCGGGCAACCCCGCGATGCCGCG 66
QY 73 CTCCCGCTGGCGAGCCGTGCGTCCCTGCTGGCGACGCCACTACCGCGAGGTGTCGCCG 132
Db 67 CTCCCGCTGGCGAGCCGTGCGTCCCTGCTGGCGACGCCACTACCGCGAGGTGTCGCCG 126
QY 133 TGGCCAGCTTGTGCGCGCCTGGGGCCCCAGAGGCTGGCGCTGTGACGCGGGGAGCC 192
|||||

Db 127 TGGCCAGCTTGTGCGCGCCTGGGGCCCCAGAGGCTGGCGCTGTGTGACGCGGGGAGCC 186
QY 193 CGCGGCTTTCCGCGCGCCTGTGGGCCAGTGCTGTGTGCTGCTGCCCTGGGACGCACAGCC 252
Db 187 GGGCGCTTCCGCGCGCCTGTGGGCCAGTGCTGTGTGCTGCTGCCCTGGGACGCACAGCC 246
QY 253 CGCCCCCGCGCGCCCTCTCTCCGCGAGTGCTGCTGCTGGAAGAGCTGTGGCCCGAG 312
Db 247 CGCCCCCGCGCGCCCTCTCTCCGCGAGTGCTGCTGCTGGAAGAGCTGTGGCCCGAG 306
QY 313 TGCTGACAGAGGCTGTGGGAGCGCGCGCGGAAGACGTGTGCTGCTGCGCTTCGCGCTGC 372
Db 307 TGCTGACAGAGGCTGTGGGAGCGCGCGCGGAAGACGTGTGCTGCTTCGCGCTGC 366
QY 373 TGGACGGGGCCCCGGGGGGCCCCCGAGGCTTCACACCAACGCTGCGACGTACCTGC 432
Db 367 TGGACGGGGCCCCGGGGGGCCCCCGAGGCTTCACCAACAGCTGCGCAGCTACCTGC 426
QY 433 CCAACACGCTGACCGAGCGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCGCGCG 492
Db 427 CCAACACGCTGACCGAGCGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGTCGCGCG 486
QY 493 TGGGCGACGACGTGTGTGTACCTGTGCTGGACGCTGCGCGCTTTGTGTGTGTGCTC 552
Db 487 TGGGCGACGACGTGTGTGTACCTGTGCTGGACGCTGCGCGCTTTGTGTGTGTGCTC 546
QY 553 CCAGCTGCGCTTACAGAGTGTGCGGGCGCGCGCTGTACACAGCTGCGGCTGCCACTCAG 612
Db 547 CCAGCTGCGCTTACAGAGTGTGCGGGCGCGCGCTGTACACAGCTGCGGCTGCCACTCAG 606
QY 613 CCGGCGCGCGCGCGCGCGCGCTAGTGAGACCCCGAAGCGCTGTGGATGCGAAGCGGCTGA 672
Db 607 CCGGCGCGCGCGCGCGCGCGCTAGTGAGACCCCGAAGCGCTGTGGATGCGAAGCGGCTGA 666
QY 673 ACCATAGCGTCAAGGAGGAGCGCGGGTCCCTGGGCTTGCCAGCGCCCGGGTGGAGAGG 732
Db 667 ACCATAGCGTCAAGGAGGAGCGCGGGTCCCTGGGCTTGCCAGCGCCCGGGTGGAGAGG 726
QY 733 GCGGGGCGAGTGCCAGCGCGAAGTGTGCTGTGCTGCGCAAGAGGCGCCAGGCGTGCCTCC 792
Db 727 GCGGGGCGAGTGCCAGCGCGAAGTGTGCTGTGCTGCGCAAGAGGCGCCAGGCGTGCCTCC 786
QY 793 CTGAGCGGAGCGAGCGCCGTTGGCGAGGGGTGCTGGGCCACCCGCGGAGAGCGGTG 852
Db 787 CTGAGCGGAGCGAGCGCCGTTGGCGAGGGGTGCTGGGCCACCCGCGGAGAGCGGTG 846
QY 853 GACCGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 912
Db 847 GACCGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 906
QY 913 CTTTGAGGCGTGCCTGT 972
Db 907 CTTTGAGGCGTGCCTGT 966
QY 973 ACGGGGGCCCCCATTCACATGTGGGCGCACACAGTCCCTGGGACACGCTTGTCCCGGG 1032
Db 967 ACGGGGGCCCCCATTCACATGTGGGCGCACACAGTCCCTGGGACACGCTTGTCCCGGG 1026
QY 1033 TGTACGCGAGACCAAGCACTTCTCTACTCTCAGGCGAGACAGAGAGCTGCGGCCCT 1092
Db 1027 TGTACGCGAGACCAAGCACTTCTCTACTCTCAGGCGAGACAGAGAGCTGCGGCCCT 1086
QY 1093 CTTTCTACTCAGCTCTCTGTAGAGCGCCAGCGCTGAGTGGCGGTGGAGGCTGTGAGACCA 1152
Db 1087 CTTTCTACTCAGCTCTCTGTAGAGCGCCAGCGCTGAGTGGCGGTGGAGGCTGTGAGACCA 1146
QY 1153 TCTTCTGGGTTCCAGGCGCTTGATGCAAGGAGTCCCGGAGTTGCCCGGCTGCGCC 1212
Db 1147 TCTTCTGGGTTCCAGGCGCTTGATGCAAGGAGTCCCGGAGTTGCCCGGCTGCGCC 1206
QY 1213 AGCGTACTGGCAAAATGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1272
Db 1207 AGCGTACTGGCAAAATGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1266

QY	1273	CCTACGGGGTGCCTCTCAAGACGCACCTGCCCCGCTGCGAGCTGCGGTCACCCCAGACGCC	1332
Db	1267	CCTACGGGGGTGCTCTCTCAAGACGCACCTGCCCCGCTGCGAGCTGCGGTCACCCCAGACGCC	1326
QY	1333	GTGTCTGTGCCCCGGAGAAACCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGACACAG	1392
Db	1327	GTGTCTGTGCCCCGGAGAAACCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGACACAG	1386
QY	1393	ACCCCCGTGCGCTGTGTGACAGCTGCTCCGCCAGCACAGACACCCCTGGCAGGTGTACGGCT	1452
Db	1387	ACCCCCGTGCGCTGTGTGACAGCTGCTCCGCCAGCACAGACACCCCTGGCAGGTGTACGGCT	1446
QY	1453	TGCTGCGGGCCCTGCGCTGCGCGGGCTGTGTGCCCCCAGCGCTCTGGGGCTCCAGGCACAGC	1512
Db	1447	TGCTGCGGGCCCTGCGCTGCGCGGGCTGTGTGCCCCCAGCGCTCTGGGGCTCCAGGCACAGC	1506
QY	1513	AACGCCGCTTCTCTCAGAAACACCAGAAGTTCACTCTCCCTGGGGGAAGCATGCCAAGCTCT	1572
Db	1507	AACGCCGCTTCTCTCAGAAACACCAGAAGTTCACTCTCCCTGGGGGAAGCATGCCAAGCTCT	1566
QY	1573	CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGCGTGCGCAGAGACC	1632
Db	1567	CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGCGTGCGCAGAGACC	1626
QY	1633	CAGGGGTTGGCTGTGTTCGGGGCCCGAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAACT	1692
Db	1627	CAGGGGTTGGCTGTGTTCGGGGCCCGAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAACT	1686
QY	1693	TCCCTGCACCTGGCTGATGAGTGTGTACGTGCTGCAGCTGCTCAAGTCTTTCTTTATGTCA	1752
Db	1687	TCCCTGCACCTGGCTGATGAGTGTGTACGTGCTGCAGCTGCTCAAGTCTTTCTTTATGTCA	1746
QY	1753	CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGT	1812
Db	1747	CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGT	1806
QY	1813	TGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCCGAAG	1872
Db	1807	TGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCCGAAG	1866
QY	1873	CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCGCGCTGCTGACGTCCAGACTCCGCTTCA	1932
Db	1867	CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCGCGCTGCTGACGTCCAGACTCCGCTTCA	1926
QY	1933	TCCCCAAGCCTGACGGGCTGCGGGCCGATTGTGAACATGCACTACGTCTGGGAGCCAGAA	1992
Db	1927	TCCCCAAGCCTGACGGGCTGCGGGCCGATTGTGAACATGCACTACGTCTGGGAGCCAGAA	1986
QY	1993	CGTTCGCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAAGGTGAAGGCACCTGTTCAAGC	2052
Db	1987	CGTTCGCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAAGGTGAAGGCACCTGTTCAAGC	2046
QY	2053	TGCTCAACTACGAGCGGGGGCGGGCCCCCGGCGCTCTGTGGCGGCCCTGTGTGGGCGCTGG	2112
Db	2047	TGCTCAACTACGAGCGGGGGCGGGCCCCCGGCGCTCTGTGGCGGCCCTGTGTGGGCGCTGG	2106
QY	2113	ACGATATCCACAGAGGCGCTGCGGCACCTTGTGTGTGCTGTGCGGGCCAGGAGCCGCGCC	2172
Db	2107	ACGATATCCACAGAGGCGCTGCGGCACCTTGTGTGTGCTGTGCGGGCCAGGAGCCGCGCC	2166
QY	2173	CTGAGCTGTA-----CATCCCCAGAGACA	2196
Db	2167	CTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGGCTTAAGACACCATCCCCAGAGACA	2226
QY	2197	GGCTCAGGAGGTCAATCGCCAGCATCATCAAAACCCAGAAACACGTACTGCGTGCCTCGGT	2256
Db	2227	GGCTCAGGAGGTCAATCGCCAGCATCATCAAAACCCAGAAACACGTACTGCGTGCCTCGGT	2286
QY	2257	ATGCCGTGGTCCAGAAAGCCGCCCATGGGCACGTCGCGAAGGCCCTTCAAGAGCCACGTCT	2316
Db	2287	ATGCCGTGGTCCAGAAAGCCGCCCATATGGGCACGTCGCGAAGGCCCTTCAAGAGCCACGTCT	2346

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Db 3427 CCTCAGACTTCAAGAACCATCTCTGGACTGATGGCCACCCGCCACAGCCAGCGCGAGAGCA 3486
QY 3457 GACACCAAGCAGCCCTGTACAGCCGGGCTCTACGTCGCCAGGAGGAGGGCGGCCACAC 3516
Db 3487 GACACCAAGCAGCCCTGTACAGCCGGGCTCTACGTCGCCAGGAGGAGGGCGGCCACAC 3546
QY 3517 CCAGGCCCGCACCCTGGAGCTGAGGCGCTGAGTGTGTCGCGGAGGCGCTGCATGT 3576
Db 3547 CCAGGCCCGCACCCTGGAGCTGAGGCGCTGAGTGTGTCGCGGAGGCGCTGCATGT 3606
QY 3577 CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGAGGGCTGAGTG 3636
Db 3607 CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGAGGGCTGAGTG 3666
QY 3637 TCCAGCACACCTGCCGCTTTCACCTTCCCCACAGGCTGCGGCTCGGCTCCACCCACAGGCGC 3696
Db 3667 TCCAGCACACCTGCCGCTTTCACCTTCCCCACAGGCTGCGGCTCGGCTCCACCCACAGGCGC 3726
QY 3697 AGCTTTCTCTACACAGAGCGCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA 3756
Db 3727 AGCTTTCTCTACACAGAGCGCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA 3786
QY 3757 TTCGCCATTGTTCACCCCTCGCCCTTGCCCTTTCACCCCGCCACCATCCAGGTG 3816
Db 3787 TTCGCCATTGTTCACCCCTCGCCCTTGCCCTTTCACCCCGCCACCATCCAGGTG 3846
QY 3817 GAGACCTTGAGAGGAGCCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCCCTG 3876
Db 3847 GAGACCTTGAGAGGAGCCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCCCTG 3906
QY 3877 TACACAGGCGAGAGCCTTGACCTGATGGGGGTCCCTGTGGGTCAAAATTGGGGGAGGT 3936
Db 3907 TACACAGGCGAGAGCCTTGACCTGATGGGGGTCCCTGTGGGTCAAAATTGGGGGAGGT 3966
QY 3937 GCTGTGGAGTAATAATACTGAATATATGAGTTTTTTCAGTTTTTGAAAAA 3996
Db 3967 GCTGTGGAGTAATAATACTGAATATATGAGTTTTTTCAGTTTTTGAAAAA 4026
QY 3997 A 3997
Db 4027 A 4027

RESULT 12
AAA29388
ID AAA29388 standard; cDNA; 4027 BP.
XX AC AAA29388;
XX 12-SEP-2000 (first entry)
DT hEST2, a human telomerase catalytic subunit homologue cDNA.
DE hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
XX retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW proliferation; immortal; tumour therapy; macular degeneration; activator;
KW INK4; ss.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 57..3455
FT /tag= a
FT /product= human_telomerase_catalytic_subunit
XX NO200031238-A2.
XX PD 02-JUN-2000.
XX PF 24-NOV-1999; 99MO-US27907.
XX PR 25-NOV-1998; 98US-0109891.

PR 17-FEB-1999; 99US-0120549.
XX (GENE-) GENETICA INC.
PA Hannon GJ, Beach DH;
XX WPI; 2000-400055/34.
DR P-PSDB; AAY96566.
XX New method for increasing the proliferative capacity of cell lines
PT comprises administering agents reversibly activating telomerase
PT activity and reversibly inactivating Rb/INK4 and/or p53 pathways useful
PT in treating age related diseases

Claim 14; Page 112-116; 123pp; English.
PS This cDNA, designated hEST2, is a human telomerase catalytic subunit
XX homologue of yeast EST2p and Euplotes p123. hEST2 is a member of the
CC reverse transcriptase family of enzymes.
CC The invention concerns methods and reagents for extending the life-span,
CC e.g. the number of mitotic divisions, of a cell. The method relies on
CC activation of a telomerase activity and inhibition of one or both of a
CC retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb
CC by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC division cycle. Binding of INK4 family members, e.g. the tumour
CC suppressor p16INK4a, inhibits kinase activity and results in growth
CC arrest. Rb inactivators can selectively and reversibly inactivate an
CC Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC and can also be used in the methods. Other molecules which can be used
CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC differs from at one or more of residues K22, R24, H95 and/or D97.
CC Additional constructs include a papilloma virus E7 protein, or other
CC viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC the Rb and p16INK4a genes may also be used. The methods are useful for
CC increasing the proliferative capacity of cells. The cells are
CC subsequently of use in pharmaceutical and cosmetic preparations used to
CC treat conditions related to (premature) ageing, e.g. macular degeneration
CC and arteriosclerosis. The cells can also be used to replace tumour cell
CC lines in vitro and for studies on biochemical and physiological aspects
CC of growth and differentiation. Long lived (immortal) cells could also be
CC of use in the production of normal or genetically engineered
CC biotechnology products.

Sequence 4027 BP; 674 A; 1361 C; 1277 G; 715 T; 0 other;

Query Match 99.0%; Score 3967; DB 21; Length 4027;
Best Local Similarity 99.0%; Pred. No. 1.1e-146;
Matches 3980; Conservative 0; Mismatches 5; Indels 36; Gaps 1;
QY 13 GCTGCTTCCTGCTGGCAGCTGGGAGAGCCCTGGCCCCCGGCCACCCCGGATGCCGCGG 72
Db 7 GCGTGCTTCCTGCTGGCAGCTGGGAGAGCCCTGGCCCCCGGCCACCCCGGATGCCGCGG 66
QY 73 CTCGCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGTCGCCG 132
Db 67 CTCGCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGTCGCCG 126
QY 133 TGGCCACGTTGCTGGCGCGCCTGGGGGCCCCAGGGCTGGCGCTGTGCAAGCGCGGACCC 192
Db 127 TGGCCACGTTGCTGGCGCGCCTGGGGGCCCCAGGGCTGGCGCTGTGCAAGCGCGGACCC 186
QY 193 CGGCGCTTTCGCGCGCTGTGCGCCAGTGCCCTGGTGTGCTGCGCTGCGCGAGCGAGGC 252
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QY 253 CGCCCCCGCGCGCCCTCTCTCCGCGCAGGTGTCTGCTGCAAGGAGCTGTGCGCGAG 312
Db 247 CGCCCCCGCGCGCCCTCTCTCCGCGCAGGTGTCTGCTGCAAGGAGCTGTGCGCGAG 306
QY 313 TGCTGAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCGCTTGCAGCTTGCAGCTGC 372
Db 307 TGCTGAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCGCTTGCAGCTTGCAGCTGC 366

QY	373	TGACGGGGCCCCGGGGGGCCCCCGAGGCCCTTCAACCACGAGGTGCAGCTACTGC	432
Db	367	TGGACGGGGCCCCGGGGGGCCCCCGAGGCCCTTCAACCACGAGGTGCAGCTACTGC	426
QY	433	CCAAACAGGTGACCGCAGCACTGCGGGGAGCGGGGCTGGGGGCTGCTGCGCCGCG	492
Db	427	CCAACACGGTGACCGCAGCACTGCGGGGAGCGGGGCTGCTGTTGCGCCGCG	486
QY	493	TGGCGCAGCAGTGCTGTCTCACCTGTGGCACGCTGCGCCCTCTTGTGCTGTGCTTC	552
Db	487	TGGCGCAGCAGTGCTGTCTCACCTGTGGCACGCTGCGCCCTCTTGTGCTGTGCTTC	546
QY	553	CCAGCTGCGCCTACCAAGTGTGCGGGCCGCGCTGTACAGCTCGGCGCTGCCATCAGG	612
Db	547	CCAGCTGCGCCTACCAAGTGTGCGGGCCGCGCTGTACAGCTCGGCGCTGCCATCAGG	606
QY	613	CCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCGTGA	672
Db	607	CCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCGTGA	666
QY	673	ACCATAGCGTCAAGGAGGCGGGGGTCCCCCTGGGCTTGCCAGCCCCGGGTGCGAGGAGGC	732
Db	667	ACCATAGCGTCAAGGAGGCGGGGGTCCCCCTGGGCTTGCCAGCCCCGGGTGCGAGGAGGC	726
QY	733	GCGGGGGCAGTGCAGCCGAGAAGTCTGCCGTTGCCCAAGAGGCCAGGCGTGGCGCTGCC	792
Db	727	GCGGGGGCAGTGCAGCCGAGAAGTCTGCCGTTGCCCAAGAGGCCAGGCGTGGCGCTGCC	786
QY	793	CTGAGCCGGAGCGGACGCGCCGTTGGGACAGGGGTCTGGGCCCACCGGGACGAGCGGTG	852
Db	787	CTGAGCCGGAGCGGACGCGCCGTTGGGACAGGGGTCTGGGCCCACCGGGACGAGCGGTG	846
QY	853	GACCGAGTGACCGTGTGTCTGTGTGTGTGTACACTGCCAGACCCGCGAAGAAGCCACTT	912
Db	847	GACCGAGTGACCGTGTGTCTGTGTGTGTGTACACTGCCAGACCCGCGAAGAAGCCACTT	906
QY	913	CTTTGGAGGGTGCGCTCTCTGTGGACGCGCCACTCCACCCATCCGTGGGCGGCAGCACC	972
Db	907	CTTTGGAGGGTGCGCTCTCTGTGGACGCGCCACTCCACCCATCCGTGGGCGGCAGCACC	966
QY	973	ACGCGGGGGCCCCCATCCACATCGGGGGCCACCAAGTCCCCTGGGACACGCCCTGTCCCCGG	1032
Db	967	ACGCGGGGGCCCCCATCCACATCGGGGGCCACCAAGTCCCCTGGGACACGCCCTGTCCCCGG	1026
QY	1033	TGTACGCGCGAGACCAAGCACTTCTTACTCTCTCAGCGCACAAGAGCAGCTGCGGCCCT	1092
Db	1027	TGTACGCGCGAGACCAAGCACTTCTTACTCTCTCAGCGCACAAGAGCAGCTGCGGCCCT	1086
QY	1093	CCTTCCCTACTCAGCTCTCTGTAGGGCCCCAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCA	1152
Db	1087	CCTTCCCTACTCAGCTCTCTGTAGGGCCCCAGCCTGACTGGCGCTCGGAGGCTCGTGAGACCA	1146
QY	1153	TCTTTCCTGGGTTCCAGGGCCCTGGATGCCAGGGACTCCCCGCAAGTTGCCCCGCTGCCCC	1212
Db	1147	TCTTTCCTGGGTTCCAGGGCCCTGGATGCCAGGGACTCCCCGCAAGTTGCCCCGCTGCCCC	1206
QY	1213	AGCGCTACTGGCAAATGCGGCCCCCTGTTTCTGGAGCTGCTGGGAACCAAGCGCAGTGCC	1272
Db	1207	AGCGCTACTGGCAAATGCGGCCCCCTGTTTCTGGAGCTGCTGGGAACCAAGCGCAGTGCC	1266
QY	1273	CCTACGGGGGTGCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCG	1332
Db	1267	CCTACGGGGGTGCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCG	1326
QY	1333	GTTGTTGTGCCCCGGAGAGCCCCCAGGGCTCTGTGGCGGCCCCCGAGAGAGACACAG	1392
Db	1327	GTTGTTGTGCCCCGGAGAGCCCCCAGGGCTCTGTGGCGGCCCCCGAGAGAGACACAG	1386
QY	1393	ACCCCCGTGCGCTGTGTGACGCTCTCCGCGACAGCACAGACGCCCTGGCAGGTGTACGGCT	1452
Db	1387	ACCCCCGTGCGCTGTGTGACGCTCTCCGCGACAGCACAGACGCCCTGGCAGGTGTACGGCT	1446

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QY	1573	CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACCTGCGCTTGCGTCAGAGACC	1632
Db	1567	CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGCGCTGCGCTTGCGTCAGAGACC	1626
QY	1633	CAGGGGTTGGCTGTGTTCGGCGCCAGAGCACCGCTCTGCGTAGAGATCCTGGCCAAGT	1692
Db	1627	CAGGGGTTGGCTGTGTTCGGCGCCAGAGCACCGCTCTGCGTAGAGATCCTGGCCAAGT	1686
QY	1693	TCCTGCACCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAAGTCTTCTTTATGTCA	1752
Db	1687	TCCTGCACCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAAGTCTTCTTTATGTCA	1746
QY	1753	CGGAGACCACGTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGTGTCTGGAGCAAGT	1812
Db	1747	CGGAGACCACGTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGTGTCTGGAGCAAGT	1806
QY	1813	TGCAAAAGCATTTGAATCAGACACCACTTGAAGAGGGTGCAGCTGCGGAGCTGTCCGAAG	1872
Db	1807	TGCAAAAGCATTTGAATCAGACACCACTTGAAGAGGGTGCAGCTGCGGAGCTGTCCGAAG	1866
QY	1873	CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCCGCCCTGCTGACGTCCAGACTCCGCTTCA	1932
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QY	1933	TCCCCAAGCCTGACGGGCTCGCGCCGATTTGTGAACATGGACTACGTCTGGGAGCCAGAA	1992
Db	1927	TCCCCAAGCCTGACGGGCTCGCGCCGATTTGTGAACATGGACTACGTCTGGGAGCCAGAA	1986
QY	1993	CGTTCCCGCAGAGAAAAGAGGGCGCCGAGCGTCTCACCTCGAGGGTGAAGGCACACTGTTACGC	2052
Db	1987	CGTTCCCGCAGAGAAAAGAGGGCGCCGAGCGTCTCACCTCGAGGGTGAAGGCACACTGTTACGC	2046
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QY	2113	ACGATATCCACAGGGGCGCTGCGCACTTCTGTGCTGCTGTGCGGGCCCCAGGACCCGCGC	2172
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QY	2173	CTGAGCTGTA-----CATCCCCCAGGACA	2196
Db	2167	CTGAGCTGTA-----CATCCCCCAGGACA	2226
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QY	2437	GCCCTCTTCGACGCTCTCTCTACGCTTTCATGTGCCACCAAGCCGCTGGCCATCAGGGGCAAGT	2496
Db	2467	GCCCTCTTCGACGCTCTCTCTACGCTTTCATGTGCCACCAAGCCGCTGGCCATCAGGGGCAAGT	2526
QY	2497	CCTACGTCAGTGCAGGGGATCCGCGAGGGGCTCCATCCTCTCTCCACGCTGTCTTCAGGCC	2556

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QY 3637 TCCAGCACACCTGCGGCTTTCACCTTCCCCACAGGCTGGCGCTCGGCTCCACCCAGGGCC 3696
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QY 3937 GCTGTGGAGTAAATACGATATATAGTTTTTCAGTTTGAAGAAAAA 3996
Db 3967 GCTGTGGAGTAAATACGATATATAGTTTTTCAGTTTGAAGAAAAA 4026
QY 3997 A 3997
Db 4027 A 4027

RESULT 13
AAAX18254
ID AAAX18254 standard; DNA; 3964 BP.
XX
XX AAX18254;
XX
DT 26-JUL-1999 (first entry)
XX
DE Human telomerase coding sequence.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation; ss.
XX
OS Homo sapiens.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US13835.
XX
PR 09-SEP-1997; 97US-0058287.
PR 01-JUL-1997; 97US-0051410.
PR 21-JUL-1997; 97US-0053018.
PR 21-JUL-1997; 97US-0053329.
PR 04-AUG-1997; 97US-0054642.
XX
PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Bowtell D, Kilian A;
XX
DR WPI; 1999-106060/09.
DR P-PSDB; AAY00627.
XX
PT New isolated vertebrate telomerase genes - used to develop products
PT for treating cancers or for organ regeneration, nerve cell or brain
PT cell growth following injury or bone marrow transplantation
XX
PS Claim 3; Fig 1; 134bp; English.
XX

Db 1861 CTCGCTTCATCCCCAAGCCTGACGGGCTGGGCCGATGTGACATGGACTACGTCGTG 1920
QY 1983 GGAGCCAGAACTTCGCGACAGAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGCA 2042
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Db 2941 AAGTGTACAGCCTGTTCTGTGATTTGCAGGCTGAACAGCCTCCAGAGGCTGTGCACCAAC 3000
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Db 3481 CGGCCACACACCAGGCGCGCCGACCGCTGGAGTCTGAGGCGCTGAGTGAATGTTTGCGCCAG 3540
QY 3567 GCCTGATGTCCCGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCG 3626
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Db 3601 GGGCTAGTGTCCAGACACACCTGCGCTTTCACTTCCACACAGGCTGGCGCTCGGCTCCA 3660
QY 3687 CCCCAGGGCCAGCTTTTCTCAACAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTC 3746
Db 3661 CCCCAGGGCCAGCTTTTCTCAACAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTC 3720
QY 3747 CATCCCCAGATTCGCCATTGTTCACCCCTGCGCCCTGCTTGCCTTCCACCCCCAC 3806
Db 3721 CATCCCCAGATTCGCCATTGTTCACCCCTGCGCCCTGCTTGCCTTCCACCCCCAC 3780
QY 3807 CATCCAGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTGTGGGAATTTGGAAGTGAACCAAG 3866
Db 3781 CATCCAGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTGTGGGAATTTGGAAGTGAACCAAG 3840
QY 3867 GTGTGCCCTGTACACAGGCGAGAGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAT 3926
Db 3841 GTGTGCCCTGTACACAGGCGAGAGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAT 3900
QY 3927 GGGGAGGTTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAGAAAAA 3986
Db 3901 GGGGAGGTTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAGAAAAA 3960
QY 3987 AAAA 3990
Db 3961 AAAA 3964
RESULT 14
AAx18269

ID AAX18269 standard; DNA; 3918 BP.
 XX AAX18269;
 AC
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE Telomerase coding sequence lacking motif A.
 XX
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W09901560-A1.
 XX
 PD 14-JAN-1999.
 XX
 PF 01-JUL-1998; 98WO-US13835.
 XX
 PR 09-SEP-1997; 97US-0058287.
 PR 01-JUL-1997; 97US-0051410.
 PR 21-JUL-1997; 97US-0053018.
 PR 21-JUL-1997; 97US-0053329.
 PR 04-AUG-1997; 97US-0054642.
 XX
 PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX
 PI Bowtell D, Kilian A;
 XX
 DR WPI; 1999-106060/09.
 DR P-PSDB; AAY00641.
 XX
 XX
 PT New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX
 PS Claim 4; Fig 11n-o; 134pp; English.
 XX
 CC This sequence encodes a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas,
 CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as
 CC Wilm's tumour, organ regeneration or differentiation after injury or
 CC diseases, nerve cell or brain cell growth following injury.
 CC Note: the 3' end of this sequence can be replaced by the sequence
 CC shown in AAX18282.
 XX
 SQ Sequence 3918 BP; 645 A; 1326 C; 1244 G; 703 T; 0 other;
 . Query Match 97.6%; Score 3910; DB 20; Length 3918;
 Best Local Similarity 99.9%; Pred. No. 1.8e-144;
 Matches 3913; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 121 CGCGGGAGACCGGGGCTTCCGGCGCGCTGTGCGCCAGTGCCCTGTGTGCGTGCCTCG 180
 QY 243 GACGCACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 302
 Db 181 GACGCACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 QY 303 GTGGCCCGAGTGTCTGACAGAGGCTGTGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 362
 Db 241 GTGGCCCGAGTGTCTGACAGAGGCTGTGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 300
 QY 363 TTGCGGCTGTGAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 422
 Db 301 TTGCGGCTGTGAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 QY 423 AGCTACCTGCCCAACACAGCTGACCGACGCTGCGGGGAGCGGGGCGTGGGCGCTGCTG 482
 Db 361 AGCTACCTGCCCAACACAGCTGACCGACGCTGCGGGGAGCGGGGCGTGGGCGCTGCTG 420
 QY 483 CTGCGCGCGGTGGGCGAGCAGCTGCTGTTACCTGCTGGCACGCTGCGGCGCTTTGTG 542
 Db 421 CTGCGCGCGGTGGGCGAGCAGCTGCTGTTACCTGCTGGCACGCTGCGGCGCTTTGTG 480
 QY 543 CTGCTGGCTCCACGCTGCGGCTTACCAGGTGTGCGGGCGGCGGCGGCTGTACCAGCTCGGCGCT 602
 Db 481 CTGCTGGCTCCACGCTGCGGCTTACCAGGTGTGCGGGCGGCGGCGGCTGTACCAGCTCGGCGCT 540
 QY 603 GCCACTCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 662
 Db 541 GCCACTCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 QY 663 CGGCGCTGGAACCATAGCGTACGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 722
 Db 601 CGGCGCTGGAACCATAGCGTACGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
 QY 723 CGGAGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 782
 Db 661 CGGAGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
 QY 783 GCGCGCTGCCCTGAGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 842
 Db 721 GCGCGCTGCCCTGAGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 QY 843 AGGACGCGTGAGCGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 902
 Db 781 AGGACGCGTGAGCGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
 QY 903 GAAGCCACTCTTTGAGAGGCTGCGCTCTGTGGCAGCGGCGGCGGCGGCGGCGGCGG 962
 Db 841 GAAGCCACTCTTTGAGAGGCTGCGCTCTGTGGCAGCGGCGGCGGCGGCGGCGGCGG 900
 QY 963 CGCCAGACACACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1022
 Db 901 CGCCAGACACACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
 QY 1023 TGTCCCCCGGTGTAGCGCGGAGACCAAGCACTTCTTACTCTCCTCAGGCGAGAGGAG 1082
 Db 961 TGTCCCCCGGTGTAGCGCGGAGACCAAGCACTTCTTACTCTCCTCAGGCGAGAGGAG 1020
 QY 1083 CTGCGGCGCTCTTCTTACTCAGCTCTGTGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1142
 Db 1021 CTGCGGCGCTCTTCTTACTCAGCTCTGTGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
 QY 1143 GTGAGACCATTTTGTGGGTTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1202
 Db 1081 GTGAGACCATTTTGTGGGTTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
 QY 1203 CGCCTGCCCGAGCGCTACTGCGCAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1262
 Db 1141 CGCCTGCCCGAGCGCTACTGCGCAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
 QY 1263 GCGCAGTGCCCTACGGGGTGTCTCTAAGACGCACTGCCCGCTGCGAGCTGGGGTAC 1322
 Db 1263 GCGCAGTGCCCTACGGGGTGTCTCTAAGACGCACTGCCCGCTGCGAGCTGGGGTAC 1322

Db 1201 GCGCAGTGCCCCCTACGGGGTGTCTCTCAAGACGCACGTGCCCGCTGGAGCTGGGTCACC 1260
QY 1323 CCAGCAGCCGGGTGTCTGTGCCCCGGGAGAACCCCCAGGGGTCTGTGGCGGCCCCCGAGAG 1382
Db 1261 CCAGCAGCCGGGTGTGTGTGCCCCGGGAGAACCCCGAGGGGTCTGTGGCGGCCCCCGAGAG 1320
QY 1383 GAGGACACAGACCCCGGTGCGCTGTGTGACGTGCTCCGCCAGACAGACGCCCTGGCAG 1442
Db 1321 GAGGACACAGACCCCGGTGCGCTGTGTGACGTGCTCCGCCAGACAGACGCCCTGGCAG 1380
QY 1443 GTGTACGGCTTCGTGGGGGCTTGCCTGCGCGCGGTGGTGGCCCCAGGCCCTGTGGGCTCC 1502
Db 1381 GTGTACGGCTTCGTGGGGGCTTGCCTGCGCGCGGTGGTGGCCCCAGGCCCTGTGGGCTCC 1440
QY 1503 AGGCACACGAACGCCGCTTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCAT 1562
Db 1441 AGGCACACGAACGCCGCTTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCAT 1500
QY 1563 GCCAAGCTCTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGTGGGGACTGGCCTTGGCTG 1622
Db 1501 GCCAAGCTCTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGTGGGGACTGGCCTTGGCTG 1560
QY 1623 CGCAGAGCCCCAGGGTGTGGCTGTGTTCGCGCCGAGAGCACCCTCTGCTGAGAGATTC 1682
Db 1561 CGCAGAGCCCCAGGGGTGTGGCTGTGTTCGCGCCGAGAGCACCCTCTGCTGAGAGATTC 1620
QY 1683 CTGGCCAAAGTTCCTGCACCTGGCTGATGATGTGTACGTCTGTCAGCTGCTCAGGTTTC 1742
Db 1621 CTGGCCAAAGTTCCTGCACCTGGCTGATGATGTGTACGTCTGTCAGCTGCTCAGGTTTC 1680
QY 1743 TTTTATGTACGGAGACCACTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTTC 1802
Db 1681 TTTTATGTACGGAGACCACTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTTC 1740
QY 1803 TGGAGCAAGTTCGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAG 1862
Db 1741 TGGAGCAAGTTCGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAG 1800
QY 1863 CTGTGGAAGCAGAGGTTCAGGACGACGATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGA 1922
Db 1801 CTGTGGAAGCAGAGGTTCAGGACGACGATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGA 1860
QY 1923 CTCCGCTTCATCCCCAAGCCTGACGGGCTGGCGCGATTGTGAACATGAGTACGTCTG 1982
Db 1861 CTCCGCTTCATCCCCAAGCCTGACGGGCTGGCGCGATTGTGAACATGAGTACGTCTG 1920
QY 1983 GGAGCCAGAAGCTTCCGACAGAAAAGAGGGCGGAGCGTCTCACCTCGAGGGTGAAGCA 2042
Db 1921 GGAGCCAGAAGCTTCCGACAGAAAAGAGGGCGGAGCGTCTCACCTCGAGGGTGAAGCA 1980
QY 2043 CTGTTACGGGTGCTCAACTACGAGCGGGCGCGCGCCCTCTTGCGGCCCTCTGTG 2102
Db 1981 CTGTTACGGGTGCTCAACTACGAGCGGGCGCGCGCCCTCTTGCGGCCCTCTGTG 2040
QY 2103 CTGGGCTTGAGCATATCCACAGGGGCTGGGCACTTCGTGCTGCGGTGTGCGGGCCAG 2162
Db 2041 CTGGGCTTGAGCATATCCACAGGGGCTGGGCACTTCGTGCTGCGGTGTGCGGGCCAG 2100
QY 2163 GACCCGCGCCTGAGCTGTACATCCCCAGGACAGGCTCACGGAAGTCAATCGCCAGCATC 2222
Db 2101 GACCCGCGCCTGAGCTGTACTTTGTCAAGGACAGGCTCACGGAAGTCAATCGCCAGCATC 2160
QY 2223 ATCAAAACCCAGAACACGTACTGCGTGTGCGGTGCGGTATGCCGTGGTCCAGAACGCCCAT 2282
Db 2161 ATCAAAACCCAGAACACGTACTGCGTGTGCGGTGCGGTATGCCGTGGTCCAGAACGCCCAT 2220
QY 2283 GGGCAGCTCCGAAGGCTTCAAGAGCCACGTCCTACCTTGACAGACCTCCAGCCGTAC 2342
Db 2221 GGGCAGCTCCGAAGGCTTCAAGAGCCACGTCCTACCTTGACAGACCTCCAGCCGTAC 2280
QY 2343 ATGCGACAGTTGTTGGCTCACTGCGAGAGAGACCGCCGCTGAGGGATGCCGTGTCATC 2402
Db 2281 ATGCGACAGTTGTTGGCTCACTGCGAGAGAGACCGCCGCTGAGGGATGCCGTGTCATC 2340

QY 2403 GAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCAGAGTCTCTCAGCCTTC 2462
Db 2341 GAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCAGAGTCTCTCAGCCTTC 2400
QY 2463 ATGTGCCACCAAGCCGCTGGCGCATCAGGGGCAAGTCTACGTCCAGTGGCCAGGGGATCCC 2522
Db 2401 ATGTGCCACCAAGCCGCTGGCGCATCAGGGGCAAGTCTACGTCCAGTGGCCAGGGGATCCC 2460
QY 2523 CAGGGCTCAATCCTCTCCACGCTGCTGTGACGCTGTGCTACAGCGACATGAGAACAG 2582
Db 2461 CAGGGCTCAATCCTCTCCACGCTGCTGTGACGCTGTGCTACAGCGACATGAGAACAG 2520
QY 2583 CTGTTTGGGGGATTTGGGGGGAGCGGCTGCTCTGCGCTTTGGTGGATGATTTCTGTTG 2642
Db 2521 CTGTTTGGGGGATTTGGGGGGAGCGGCTGCTCTGCGCTTTGGTGGATGATTTCTGTTG 2580
QY 2643 GTGACACCTCACCCTCACCCACGCGAAAACCTTCTCAGGACCCTGTGTCGAGGTGCCCT 2702
Db 2581 GTGACACCTCACCCTCACCCACGCGAAAACCTTCTCAGGACCCTGTGTCGAGGTGCCCT 2640
QY 2703 GAGTATGGCTGCGTGTGTGAACCTTGGGAGACAGAGTGTGAACCTTCCCTGTAGAAGACGAG 2762
Db 2641 GAGTATGGCTGCGTGTGTGAACCTTGGGAGACAGAGTGTGAACCTTCCCTGTAGAAGACGAG 2700
QY 2763 GGCCTGGGTGACAGGGCTTTGTTGACATGCGCGGCCACAGGCGCTATTCCTCGTGGCGG 2822
Db 2701 GGCCTGGGTGACAGGGCTTTGTTGACATGCGCGGCCACAGGCGCTATTCCTCGTGGCGG 2760
QY 2823 CTGCTGTGATACCCCGAACCTTGAGGTGCAGAGGACTACTCCAGCTATGCGCGGACC 2882
Db 2761 CTGCTGTGATACCCCGAACCTTGAGGTGCAGAGGACTACTCCAGCTATGCGCGGACC 2820
QY 2883 TCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCCG 2942
Db 2821 TCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCCG 2880
QY 2943 AAACCTTTTGGGGTCTTGGCGCTGAAGTGTCAACAGCCTGTTCTGAGTTTGCAGGTGAAC 3002
Db 2881 AAACCTTTTGGGGTCTTGGCGCTGAAGTGTCAACAGCCTGTTCTGAGTTTGCAGGTGAAC 2940
QY 3003 AGCCTCCAGAGGGTGTGCACCAACATCTAACAGATTCCTCTGCTCAGGCGTACAGTTT 3062
Db 2941 AGCCTCCAGAGGGTGTGCACCAACATCTAACAGATTCCTCTGCTCAGGCGTACAGTTT 3000
QY 3063 CACGCATGTGTGCTGACGTCCCATTTTCATCAGCAAGTTTGAAGAACCCACATTTTTC 3122
Db 3001 CACGCATGTGTGCTGACGTCCCATTTTCATCAGCAAGTTTGAAGAACCCACATTTTTC 3060
QY 3123 CTGGCGGTCAATCTGACACGGGCTCCCTGTCTACTCCATCTGTAAGAACCAAGAACGA 3182
Db 3061 CTGGCGGTCAATCTGACACGGGCTCCCTGTCTACTCCATCTGTAAGAACCAAGAACGA 3120
QY 3183 GGGATGTGCTGGGGGCCAAGGGCGCGCGCCCTCTGCCCTCGAGGGCGGCTGCAAGTGG 3242
Db 3121 GGGATGTGCTGGGGGCCAAGGGCGCGCGCCCTCTGCCCTCGAGGGCGGCTGCAAGTGG 3180
QY 3243 CTGTGCCACCAAGCATTTCTGCTCAAGCTGACTGACACCGGTGTACCTACGTGCCACTC 3302
Db 3181 CTGTGCCACCAAGCATTTCTGCTCAAGCTGACTGACACCGGTGTACCTACGTGCCACTC 3240
QY 3303 CTGGGGTCACTCAGAGCAGGCCAGAGCGCAGCTGAGTGGGAAGCTCCCGGGAGCAGCGCTG 3362
Db 3241 CTGGGGTCACTCAGAGCAGGCCAGAGCGCAGCTGAGTGGGAAGCTCCCGGGAGCAGCGCTG 3300
QY 3363 ACTGCCCTGAGAGCCGAGCGCAACCCGGCACTGCCCTCAGACTTCAAGACCATCTGGAC 3422
Db 3301 ACTGCCCTGAGAGCCGAGCGCAACCCGGCACTGCCCTCAGACTTCAAGACCATCTGGAC 3360
QY 3423 TGAATGGCCACCCGCCACAGCCAGGCCGAGACAGACCAAGCAGCCCTGTCAAGCCGGG 3482
Db 3361 TGAATGGCCACCCGCCACAGCCAGGCCGAGACAGACCAAGCAGCCCTGTCAAGCCGGG 3420

QY 3483 CTCTACGTCCAGGAGGAGGGGGCCACACACCCAGGCCCGCACCGCTGGAGTCTGA 3542
DB 3421 CTCTACGTCCAGGAGGAGGGGGCCACACACCCAGGCCCGCACCGCTGGAGTCTGA 3480
QY 3543 GGCCGTGAGTGTGTTGGCCGAGGCCCTGATGTCGGCTGAAGGCTGAGTGTCCGGCTG 3602
DB 3481 GGCCGTGAGTGTGTTGGCCGAGGCCCTGATGTCGGCTGAAGGCTGAGTGTCCGGCTG 3540
QY 3603 AGGCTGAGGAGTGTCCAGCCAGGGGCTGAGTGTCCAGCACACCTGCGTCTCACTTC 3662
DB 3541 AGGCTGAGGAGTGTCCAGCCAGGGGCTGAGTGTCCAGCACACCTGCGTCTCACTTC 3600
QY 3663 CCCACAGGCTGCGCTCGGCTCCACCCAGGGCCAGCTTTCTCTACAGAGGCCGCT 3722
DB 3601 CCCACAGGCTGCGCTCGGCTCCACCCAGGGCCAGCTTTCTCTACAGAGGCCGCT 3660
QY 3723 TCCACTCCACATAGGAATAGTCCATCCACAGATTCGCATGTTCACCCCTCGCCCTG 3782
DB 3661 TCCACTCCACATAGGAATAGTCCATCCACAGATTCGCATGTTCACCCCTCGCCCTG 3720
QY 3783 CCCTCCTTGCCTTCCACCCCGCACCATCCAGGTGAGAGCCCTGAGAGGACCCCTGGAGC 3842
DB 3721 CCCTCCTTGCCTTCCACCCCGCACCATCCAGGTGAGAGCCCTGAGAGGACCCCTGGAGC 3780
QY 3843 TCTGGGAATTGGAGTACCAAGGTGCGCTGTACACAGGAGGACCCCTGCACCTGG 3902
DB 3781 TCTGGGAATTGGAGTACCAAGGTGCGCTGTACACAGGAGGACCCCTGCACCTGG 3840
QY 3903 ATGGGGGTCCTGTGGTCAAAATGGGGGAGGTGCTGTGGAGTAAATACTGAATATA 3962
DB 3841 ATGGGGGTCCTGTGGTCAAAATGGGGGAGGTGCTGTGGAGTAAATACTGAATATA 3900
QY 3963 TGAGTTTTCAGTTTGA 3980
DB 3901 TGAGTTTTCAGTTTGA 3918

81np

RESULT 15
AA18278
ID AAX18278 standard; DNA; 3918 BP.
AC AAX18278;
XX 26-JUL-1999 (first entry)
DT
XX
DE Telomerase coding sequence lacking motif A.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
PD 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US13835.
PF
XX
PR 09-SEP-1997; 97US-0058287.
PR 01-JUL-1997; 97US-0051410.
PR 21-JUL-1997; 97US-0053018.
PR 21-JUL-1997; 97US-0053329.
PR 04-AUG-1997; 97US-0054642.

XX
PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Bowtell D, Kilian A;
XX
DR WPI; 1999-106060/09.
DR P-PSDB; AAY00650.

XX
PT New isolated vertebrate telomerase genes - used to develop products
PT for treating cancers or for organ regeneration, nerve cell or brain
PT cell growth following injury or bone marrow transplantation
XX
PS Claim 4; Fig 11ah-a; 134pp; English.
XX
CC This sequence encodes a truncated human telomerase of the
CC invention. Primers that amplify the telomerase coding sequence can be
CC used in a method for diagnosing cancer in a patient. The telomerase can
CC be used for detection, diagnosis and drug screening. Inhibitors of
CC telomerase activity can be used to treat cancers such as melanomas,
CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
CC or skin growths. Enhancers of telomerase may be used to stimulate stem
CC cell proliferation and differentiation (expansion of haematopoietic stem
CC cells could be administered in the bone marrow transplant context). As
CC well, many tissues have stem cells. Proliferation of these cells may be
CC useful in wound healing, hair growth, treatment of disease such as
CC Wilm's tumour, organ regeneration or differentiation after injury or
CC diseases, nerve cell or brain cell growth following injury.
CC Note: the 5' end of this sequence can be replaced by the sequence
CC shown in AAX18284.
XX
SQ Sequence 3918 BP; 645 A; 1326 C; 1244 G; 703 T; 0 other;

Query Match 97.6%; Score 3910; DB 20; Length 3918;
Best Local Similarity 99.9%; Pred. No. 1.8e-144;
Matches 3913; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 63 ATGCCGGCGGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGCAGCCTACCGCGAG 122
DB 1 ATGCCGGCGGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGCAGCCTACCGCGAG 60
QY 123 GTGCTGCCGTGCGCAGCTTCTGCGCGGCTGGGGCCCGCAGGGCTGGCGCTGTGCAG 182
DB 61 GTGCTGCCGTGCGCAGCTTCTGCGCGGCTGGGGCCCGCAGGGCTGGCGCTGTGCAG 120
QY 183 CGGGGGAGCCCGCGGCTTTCGCGCGGCTGTGGCCAGTGCCTGTGTGCTGCTGCTGG 242
DB 121 CGGGGGAGCCCGCGGCTTTCGCGCGGCTGTGGCCAGTGCCTGTGTGCTGCTGCTGG 180
QY 243 GACGACAGCG 302
DB 181 GACGACAGCG 240
QY 303 GTGGCCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 362
DB 241 GTGGCCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 363 TTCGCGCTGTGAGAGCG 422
DB 301 TTCGCGCTGTGAGAGCG 360
QY 423 AGCTACCTGCCCAACACAGGTGACCGACGCACTGGGGGGAGCGGGGCGTGGGGCTGCTG 482
DB 361 AGCTACCTGCCCAACACAGGTGACCGACGCACTGGGGGGAGCGGGGCGTGGGGCTGCTG 420
QY 483 CTGGCGCGCGGTGGGGGAGAGAGTGTGCTTCACTGCTGGACAGCTGGCGCTTTGTG 542
DB 421 CTGGCGCGCGGTGGGGGAGAGAGTGTGCTTCACTGCTGGACAGCTGGCGCTTTGTG 480
QY 543 CTGGTGGCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCTGTACCAAGCTGGCGCT 602
DB 481 CTGGTGGCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCTGTGTACCAAGCTGGCGCT 540
QY 603 GCCACTCAGCG 662
DB 541 GCCACTCAGCG 600
QY 663 CGGGCTGGAACATAGCGTACGAGGCGGGGCTCCCGCTGGCGCTGCGACGCCCGGGT 722
DB 601 CGGGCTGGAACATAGCGTACGAGGAGCGGGGCTCCCGCTGGCGCTGCGACGCCCGGGT 660

QY 723 GCGAGAGAGCGCGGGGCGAGTGCACGCCGAAGTCTGCCGTTCGCCCAAGAGGCCAGCGCT 782
DB 661 GCGAGAGAGCGCGGGGCGAGTGCACGCCGAAGTCTGCCGTTCGCCCAAGAGGCCAGCGCT 720
QY 783 GGGCGTGGCCCCGTGAGCCGGAGCGGACGCCCGTTGGGACAGGGTCTTGCGCCACCCGGGC 842
DB 721 GGGCGTGGCCCCGTGAGCCGGAGCGGACGCCCGTTGGGACAGGGTCTTGCGCCACCCGGGC 780
QY 843 AGGAGCGGTGAGCCGAGTGACCGGTGTTCTGTGTGTGTACCTTGCCAGACCCGCCGAA 902
DB 781 AGGAGCGGTGAGCCGAGTGACCGGTGTTCTGTGTGTGTACCTTGCCAGACCCGCCGAA 840
QY 903 GAAGCCACCTCTTTGGAGGGTGCCTCTGTGGACGGCCACTCCACCCTCCGTGGGC 962
DB 841 GAAGCCACCTCTTTGGAGGGTGCCTCTGTGGACGGCCACTCCACCCTCCGTGGGC 900
QY 963 CGCCAGACACACGGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGCT 1022
DB 901 CGCCAGACACACGGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGCT 960
QY 1023 TGTCCCCGGGTGTACGCCCGAGACCAAGCAGTCTCTACTCTCAGCGCAAGAGCAG 1082
DB 961 TGTCCCCGGGTGTACGCCCGAGACCAAGCAGTCTCTACTCTCAGCGCAAGAGCAG 1020
QY 1083 CTGCGCCCTCTCTCTACTACTAGCTCTCTGAGGCCACGCTGAGCTGGCGCTCGAGGCTC 1142
DB 1021 CTGCGCCCTCTCTCTACTACTAGCTCTCTGAGGCCACGCTGAGCTGGCGCTCGAGGCTC 1080
QY 1143 GTGGAGACCATCTTCTTGGGTTCAGAGGCCCTGATGCCAGGAGTCCCGCAGGTTGCC 1202
DB 1081 GTGGAGACCATCTTCTTGGGTTCAGAGGCCCTGATGCCAGGAGTCCCGCAGGTTGCC 1140
QY 1203 CGCCTGCCCCAGCGCTACTGGAATATCGGCCCTGTTCTGAGACTGTGGAACCAAC 1262
DB 1141 CGCCTGCCCCAGCGCTACTGGAATATCGGCCCTGTTCTGAGACTGTGGAACCAAC 1200
QY 1263 GCGCAGTCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCCGCTCGAGCTGCGGTAC 1322
DB 1201 GCGCAGTCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCCGCTCGAGCTGCGGTAC 1260
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DB 1261 CCAGCAGCCGGTGTCTGTGCCCCGGGAGAAAGCGGCTGTGTGGCGGGCCCCGAGAG 1320
QY 1383 GAGGACACAGACCCCGCTGCGCTGTGCAGCTGTCCGCCACACAGACAGCCCTGCGAG 1442
DB 1321 GAGGACACAGACCCCGCTGCGCTGTGCAGCTGTCCGCCACACAGACAGCCCTGCGAG 1380
QY 1443 GTGTACGGCTTGTGTGGGGCCCTGCTGCGCGGCTGTGTGCCCGGCTGTGGGCTCC 1502
DB 1381 GTGTACGGCTTGTGTGGGGCCCTGCTGCGCGGCTGTGTGCCCGGCTGTGGGCTCC 1440
QY 1503 AGGACACAGAACGCCGCTTCTCTAGGAACACCAAGAAGTTCATCTCCCTGGGGAAACAT 1562
DB 1441 AGGACACAGAACGCCGCTTCTCTAGGAACACCAAGAAGTTCATCTCCCTGGGGAAACAT 1500
QY 1563 GCCAAGCTCTGCTGCAAGAGAGTGAAGTGAAGTGAAGCGTGGGAGTGGCTTGCTG 1622
DB 1501 GCCAAGCTCTGCTGCAAGAGAGTGAAGTGAAGTGAAGCGTGGGAGTGGCTTGCTG 1560
QY 1623 CGCAGAGAGCCAGGGGTTGGCTGTGTCCGGCCGAGAGCACCGTCTGCGTGAAGATC 1682
DB 1561 CGCAGAGAGCCAGGGGTTGGCTGTGTCCGGCCGAGAGCACCGTCTGCGTGAAGATC 1620
QY 1683 CTGGCAAGTCTGCACTGGCTGATGAGTGTATGCTGCTGAGCTGCTAGGCTTTTC 1742
DB 1621 CTGGCAAGTCTGCACTGGCTGATGAGTGTATGCTGCTGAGCTGCTAGGCTTTTC 1680
QY 1743 TTTTATGTACGGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAGAGTGTTC 1802
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QY 1863 CTGTGGAAGCAGAGGTGAGGAGCATTCGGGAAGCCAGGCCCGCTGTGAGCTCCAGA 1922
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DB 2161 ATCAAAACCCAGAACACAGTACTGCGTGCCTGGTATGCCGTGTGCCAGAAAGCGCCCAT 2220
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Db 3841 ATGGGGTCCCTGTGGGTCAAAATTTGGGGGAGGTGCTGTGGAGTAAATACTGAATATA 3900
QY 3963 TGAGTTTTCAGTTTGA 3980
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Db 3901 TGAGTTTTCAGTTTGA 3918
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Job time : 841 secs

Stop.

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2003, 20:04:45 ; Search time 2769 Seconds
(without alignments)
6431.158 Million cell updates/sec

Title:	US-09-424-686B-1DEL
Perfect score:	4006
Sequence:	1 gttcagcagcgtcgtc.....aaaaaaaaaaaaaaaaaa 4006

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 5870958 seqs, 2222650499 residues

Total number of hits satisfying chosen parameters: 11741916

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3996	99.8	4042	6	US-09-424-686B-1	Sequence 1, Appli
2	3982.6	99.4	4037	6	US-09-721-456-343	Sequence 343, App
3	3982.6	99.4	4037	9	US-10-325-810-343	Sequence 343, App
4	3969	99.1	4015	1	PCT-US02-1635-1	Sequence 1, Appli
5	3969	99.1	4015	1	PCT-US02-3146-19	Sequence 19, Appli
6	3969	99.1	4015	6	US-09-721-456-1	Sequence 1, Appli
7	3969	99.1	4015	6	US-09-949-016-455	Sequence 455, App
8	3969	99.1	4015	8	US-10-388-578-1	Sequence 1, Appli
9	3969	99.1	4015	8	US-10-389-431-1	Sequence 1, Appli
10	3969	99.1	4015	9	US-10-208-243-1	Sequence 1, Appli
11	3969	99.1	4015	9	US-10-325-810-1	Sequence 1, Appli
12	3967.4	99.0	4015	8	US-10-170-235-38656	Sequence 38656, A
13	3954.2	98.7	4016	7	US-09-949-016-5841	Sequence 5841, App
14	3914.8	97.7	3964	6	US-09-108-401A-1	Sequence 1, Appli
15	3914.8	97.7	3964	6	US-09-502-498A-1	Sequence 1, Appli
16	3914.8	97.7	3964	7	US-09-502-424A-1	Sequence 1, Appli
17	3910	97.6	3918	6	US-09-108-401A-1	Sequence 1, Appli
18	3910	97.6	3918	6	US-09-502-498A-455	Sequence 45, App
19	3910	97.6	3918	7	US-09-502-424A-455	Sequence 45, App
20	3900	97.4	4022	6	US-09-108-401A-75	Sequence 75, App
21	3900	97.4	4022	6	US-09-502-498A-75	Sequence 75, App
22	3900	97.4	4022	7	US-09-502-424A-75	Sequence 75, App

23	3834.4	95.7	14952	7	US-09-949-016-12197	Sequence 12197, App
24	3834.4	95.7	44960	7	US-09-949-016-17583	Sequence 17583, App
25	3832.6	95.7	4029	6	US-09-721-456-292	Sequence 292, App
26	3832.6	95.7	4029	9	US-10-325-810-292	Sequence 292, App
27	3797	94.8	3855	6	US-09-721-456-4	Sequence 0, Appl
28	3797	94.8	3855	9	US-10-325-810-4	Sequence 4, Appl
29	3384	84.5	13766	9	US-10-105-616-1	Sequence 1, Appl
30	3362.4	83.9	8742	9	US-10-105-616-6	Sequence 6, Appl
31	3354	83.7	3453	9	US-10-205-629-1	Sequence 1, Appl
32	3346.8	83.5	3396	6	US-09-108-401A-40	Sequence 40, Appl
33	3346.8	83.5	3396	6	US-09-502-498A-40	Sequence 40, Appl
34	3346.8	83.5	3396	7	US-09-502-424A-40	Sequence 40, Appl
35	3336.8	83.3	3500	6	US-09-108-401A-63	Sequence 63, Appl
36	3336.8	83.3	3500	6	US-09-502-498A-63	Sequence 63, Appl
37	3336.8	83.3	3500	7	US-09-502-424A-63	Sequence 63, Appl
38	3149	78.6	3326	6	US-09-108-401A-49	Sequence 49, Appl
39	3149	78.6	3326	6	US-09-502-498A-49	Sequence 49, Appl
40	3147	78.6	3362	7	US-09-502-424A-49	Sequence 49, Appl
41	3147	78.6	3362	6	US-09-108-401A-43	Sequence 43, Appl
42	3147	78.6	3362	6	US-09-502-498A-43	Sequence 43, Appl
43	3147	78.6	3362	7	US-09-502-424A-43	Sequence 43, Appl
44	3140	78.4	3432	6	US-09-108-401A-83	Sequence 83, Appl
45	3140	78.4	3432	6	US-09-502-498A-83	Sequence 83, Appl

ALIGNMENTS

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RESULT 1
US-09-424-686B-1
; Sequence 1, Application US/09424686b
; GENERAL INFORMATION:
; APPLICANT: Hagen, Gustav
; APPLICANT: Siegmund, Hans-Ulrich
; APPLICANT: Weichel, Walter
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; FILE REFERENCE: Bayer 10,203
; CURRENT APPLICATION NUMBER: US/09/424,686B
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/EP98/03468
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft word
; SEQ ID NO 1
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-424-686B-1

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Query Match	99.8%;	Score 3996;	DB 6;	Length 4042;
Best Local Similarity	99.1%;	Pred. No. 6.2e-112;		
Matches 4006; Conservative	0;	Mismatches 0;	Indels 36;	Gaps 1;

[illegible]

[illegible]

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QY	1441	AGGTATACGG	CTTCGTGCGGG	CTGCTCCG	CGCGCTGGT	CGCCCCAGGCTCT	1500
Db	1441	AGGTATACGG	CTTCGTGCGGG	CTGCTCCG	CGCGCTGGT	CGCCCCAGGCTCT	1500
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RESULT 2
US-09-721-456-343
; Sequence 343, Application US/09721456
;
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;             Lingner, Joachim
;             Nakamura, Toru
;             Chapman, Karen B.
;             Morin, Gregg B.
;             Harley, Calvin B.
;             Andrews, William H.
;
;   TITLE OF INVENTION: Human telomerase Catalytic Subunit
;
;   NUMBER OF SEQUENCES: 727
;
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/721,456
;     FILING DATE: 22-Nov-2000
;     CLASSIFICATION: <Unknown>
;
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/974,549A
;     FILING DATE: 19-Nov-1997
;     APPLICATION NUMBER: US 08/724,643
;     FILING DATE: 01-Oct-1996
;     APPLICATION NUMBER: US 08/844,419
;     FILING DATE: 18-Apr-1997
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0026100S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"
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US-09-721-456-343

Query Match 99.48; Score 3982.6; DB 6; Length 4037;
Best Local Similarity 98.98; Pred. No. 1.6e-111;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;

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QY 248 ACGGCGCGCGCGCGCGCGCGCGCTCTCCCTGCGCAGGTGTCTGCTGAAGAGAGTGTGGC 307
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QY 428 CCTGCCCAACAGGCTGACCGACGCTGCGGGGAGCGGGGGCTGGGGGCTGCTGCTGCG 487
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QY 968 GCACACGCGCGCGCGCGCGCGCGCGCATTCACATGCGCGCGCACACGCTCCGGAACAGCGCTGTCC 1027
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QY 1088 GCGCTCTTCTTACTACTAGCTCTCTGAGCGCCAGCCTGACTGGCGCTCGAGGCTCTGTGA 1147
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DB 1321 AGCGGCTGTCTGTGCGCGGAGAGCGCCAGGGCTCTGTGGCGCGCGCGCGAGAGAGA 1380
QY 1388 CACAGACCCCGCTGCGCTGTGTCAGCTCTCCGCAAGCACAGCAGCCCTGGCAGTGT 1447
DB 1381 CACAGACCCCGCTGCGCTGTGTCAGCTCTCCGCAAGCACAGCAGCCCTGGCAGTGT 1440
QY 1448 CGGCTGTGCGGGCGCTGCTGCGCGCGCTGTGCGCGCGCGCGCGCTGTGGGCTCCAGGCA 1507
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QY 1508 CAACGAACGCGCTTCTCAGGAACACCAAGATTATCTCCCTGGGGAAGCATGCA 1567
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Db 1561 GCTCTGCTGCAGAGAGCTGACGTGAGAGATGAGCGTGCAGACTGCGCTTGCGTGCAG 1620
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Db 1681 CAAGTCTCTGACTGGCTGATGAGTGTGTACGTGTGAGCTGTGCTCAGGCTTTCTTTTA 1740
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RESULT 3
US-10-325-810-343

; Sequence 343, Application US/10325810
; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 633

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/325,810

; FILING DATE: 20-Dec-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/402,181

; FILING DATE: 29-Sep-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-Oct-1996

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-Apr-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-Apr-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-May-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-May-1997

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-Aug-1997

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-Aug-1997

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-Aug-1997

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-Oct-1997

; ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FEATURE:
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US-10-325-810-343

Query Match 99.4%; Score 3982.6; DB 9; Length 4037;
Best Local Similarity 98.9%; Pred. No. 1.6e-111;
Matches 3992; Conservative 4; Mismatches 3; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGGCCCGCCACCCCGGATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGGCCCGCCACCCCGGATGCC 60
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QY	2492	CAAGTCCCTACGTCACAGTGCAGAGGGATCCCGCAGAGGCTCCATCCTCTCCACGCTGCTCG	2551
Db	2521	CAAGTCCCTACGTCACAGTGCAGAGGGATCCCGCAGAGGCTCCATCCTCTCCACGCTGCTCG	2580
QY	2552	CAGCGTGTCTACGGGGCAGCATGGAGAAACAAGCTGTTGGCGGGGATTTGGCGGAGGGCT	2611
Db	2581	CAGCGTGTCTACGGGGCAGCATGGAGAAACAAGCTGTTGGCGGGGATTTGGCGGAGGGCT	2640
QY	2612	GCTCCTGCGTTTGGTGGATGATTTCTTGGTGTACACCTCACCTCAACCACGCGAAAAAC	2671
Db	2641	GCTCCTGCGTTTGGTGGATGATTTCTTGGTGTACACCTCAACCACGCGAAAAAC	2700
QY	2672	CTTCCTCAGGACCCTGTGTCGAGGTGTCCCTAGTATGGTGGTGGTGAACCTGCGGAA	2731
Db	2701	CTTCCTCAGGACCCTGTGTCGAGGTGTCCCTAGTATGGTGGTGGTGAACCTGCGGAA	2760
QY	2732	GACAGTGTGAACCTTCCCTGTAGAGACAGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGTGAACCTTCCCTGTAGAGACAGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2820
QY	2792	GCCGGCCCAAGGCTATTCCTCCTGTGTCGGGCTGCTGCTGTGATACCCGAGCCCTGGAAGT	2851
Db	2821	GCCGGCCCAAGGCTATTCCTCCTGTGTCGGGCTGCTGCTGTGATACCCGAGCCCTGGAAGT	2880
QY	2852	GCAGAGCGACTACTCAGCTATGCGCCGAGCCCATCAGAGCCAGTCTCAACTCAACCG	2911
Db	2881	GCAGAGCGACTACTCAGCTATGCGCCGAGCCCATCAGAGCCAGTCTCAACTCAACCG	2940

QY 2912 CGGCTTCAAGCTGGAGGAAACATGCGTCCAAACTCTTTGGGGTCTTGGCGCTGAAGTG 2971
Db 2941 CGGCTTCAAGCTGGAGGAAACATGCGTCCAAACTCTTTGGGGTCTTGGCGCTGAAGTG 3000
QY 2972 TCACAGCTGTTCTGGATTGTCAGGTGAACAGCTCCAGACGGGTGTGCACCAACATCTA 3031
Db 3001 TCACAGCTGTTCTGGATTGTCAGGTGAACAGCTCCAGACGGGTGTGCACCAACATCTA 3060
QY 3032 CAAGATCCTCTGCTGCAGGCGGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCATTTC 3091
Db 3061 CAAGATCCTCTGCTGCAGGCGGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCATTTC 3120
QY 3092 TCAGCAAGTTGGAAGAACCCACATTTTCTGCGCGTCATCTGTGACAGCGGCTCCCT 3151
Db 3121 TCAGCAAGTTGGAAGAACCCACATTTTCTGCGCGTCATCTGTGACAGCGGCTCCCT 3180
QY 3152 CTGCTACTCCATCTGAAAGCCAAAGACGAGGATGTGCTGGGGCCAAAGGGCGCGC 3211
Db 3181 CTGCTACTCCATCTGAAAGCCAAAGACGAGGATGTGCTGGGGCCAAAGGGCGCGC 3240
QY 3212 CGGCCCTTGCCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3271
Db 3241 CGGCCCTTGCCTCCGAGGCGGTGACGTGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGTGTACCTACGTGCACTCCTGGGGTCACTACAGACAGCCACAGCGCA 3331
Db 3301 GACTCGACACCGTGTACCTACGTGCACTCCTGGGGTCACTACAGACAGCCACAGCGCA 3360
QY 3332 GCTGAGTCGGAAGCTCCCGGGAGCAGCGCTGACTGCCCTGGAGGGCCGCAACCCGGC 3391
Db 3361 GCTGAGTCGGAAGCTCCCGGGAGCAGCGCTGACTGCCCTGGAGGGCCGCAACCCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACCCGCCACAGCCAGGCGCGA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACCCGCCACAGCCAGGCGCGA 3480
QY 3452 GAGCAGACACAGCAGCCCTGTACAGCCGGGCTTACGTCCAGGAGGAGGGGGCGCGC 3511
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QY 3512 CACACCCAGGCCCGCACCCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCTG 3571
Db 3541 CACACCCAGGCCCGCACCCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3660
QY 3632 GAGTGTCCAGACACCTGCGGCTTTCACCTTCCCCACAGAGGCTGGCGCTCGGCTCCACCCA 3691
Db 3661 GAGTGTCCAGACACCTGCGGCTTTCACCTTCCCCACAGAGGCTGGCGCTCGGCTCCACCCA 3720
QY 3692 GGGCCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3751
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QY 3752 CCAGATTCCCATTTGTTCAACCCCTGCGCTGCCCTTTCCTTCCACCCCCACCATCC 3811
Db 3781 CCAGATTCCCATTTGTTCAACCCCTGCGCTGCCCTTTCCTTCCACCCCCACCATCC 3840
QY 3812 AGGTGAGACCTTGAGAGGACCTGAGGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3871
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QY 3872 CCCTGTACACAGGCGAGGACCTGACCTGGATGGGGTCCCTGTGGGTCAAAATTGGGG 3931
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QY 3932 GAGGTGCTGTGGAGTAAATATCTGAATATAGTGTTCAGTGTGAAAAAATGAGG 3991
Db 3961 GAGGTGCTGTGGAGTAAATATCTGAATATAGTGTTCAGTGTGAAAAAATGAGG 4020

QY 3992 AAAAAAAAAAAAAA 4006
Db 4021 AAAAAAAAAAAAAA 4035

RESULT 4
PCT-US02-31635-1
; Sequence 1, Application PC/TUS0231635
; GENERAL INFORMATION:
; APPLICANT: Boston University et al.
; TITLE OF INVENTION: PREADIPOCYTE CELL STRAINS AND USES THEREFORE
; FILE REFERENCE: BUI-011PC
; CURRENT APPLICATION NUMBER: PCT/US02/31635
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327650
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/327651
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-31635-1

Query Match 99.1%; Score 3969; DB 1; Length 4015;
Best Local Similarity 99.1%; Pred. No. 3.9e-111;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCGTCTGCTGCGACGTGGGAAGCCCTGGCCCCGGCCACCCCGGATGCC 67
Db 1. GCAGCGCTGCGTCTGCTGCGACGTGGGAAGCCCTGGCCCCGGCCACCCCGGATGCC 60

QY 68 GCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGT 127
Db 61 GCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGT 120

QY 128 GCGGCTGCGCAGTTCGTGCGGCGGCTGGGGCCCCAGGGCTGGCGCTGTGACGCGG 187
Db 121 GCGGCTGCGCAGTTCGTGCGGCGGCTGGGGCCCCAGGGCTGGCGCTGTGACGCGG 180

QY 188 GGACCCGGGCGCTTTCGGCGGCTGTGCGCCAGTGCCTGTGTGCGTCCCTGGAGCG 247
Db 181 GGACCCGGGCGCTTTCGGCGGCTGTGCGCCAGTGCCTGTGTGCGTCCCTGGAGCG 240

QY 248 ACGGCG 307
Db 241 ACGGCG 300

QY 308 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGTGTGCTGCGCTTGGCG 367
Db 301 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGTGTGCTGCGCTTGGCG 360

QY 368 GCTGCTGAGCGGGGCGCGCGGGGGCGCGCGAGGCTTACACACAGCGTGGCGAGCTA 427
Db 361 GCTGCTGAGCGGGGCGCGGGGGCGCGCGAGGCTTACACACAGCGTGGCGAGCTA 420

QY 428 CCGCCCAACAGGTGACCGCAGCGCTGCGGGGGAGCGGGGGCTGCTGCTGCG 487
Db 421 CCGCCCAACAGGTGACCGCAGCGCTGCGGGGGAGCGGGGGCTGCTGCTGCG 480

QY 488 CCGCGTGGGCGAGCAGCTGTGCTGCTGCTGCTGCGACGCTGCGCGCTTGTGCTGCT 547
Db 481 CCGCGTGGGCGAGCAGCTGTGCTGCTGCTGCTGCGACGCTGCGCGCTTGTGCTGCT 540

QY 548 GGTGCTGAGCTGCGCTTACAGAGTGTGCGGGCGCGCGCTGTACAGCTGCGCGTGCAC 607
Db 541 GGTGCTGAGCTGCGCTTACAGAGTGTGCGGGCGCGCGCTGTACAGCTGCGCGTGCAC 600

QY 608 TCAGGCGCGCGCGCGCGCACAGCTGAGTGAACCCGGAAGCGCTGTGGATGCGAAGCGG 667
Db 601 TCAGGCGCGCGCGCGCGCACAGCTGAGTGAACCCGGAAGCGCTGTGGATGCGAAGCGG 660

[illegible]

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Db      3901  CCCTGTACACAGGCGAGGACCCTGCACCTGCGATGGGGGTCCCTGTGGGTCAAAATTGGGGC  3960
Oy      3932  GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGGAAAAAA  3986
          |||||||
Db      3961  GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGGAAAAAA  4015

RESULT 5
PCT-US02-33146-19
; sequence 19, Application PC/TUS0233146
; GENERAL INFORMATION:
; APPLICANT: University of Rochester Medical Center
; APPLICANT: Rowley, Peter
; TITLE OF INVENTION: Telomerase Interference
; FILE REFERENCE: FP-71506-2/RPT/SRN
; CURRENT APPLICATION NUMBER: PCT/US02/33146
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-33146-19

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Query Match	99.1%;	Score 3969;	DB 1;	Length 4015;
Best Local Similarity	99.1%;	Pred. No. 3.9e-111;		
Matches 3979;	Conservative	0;	Mismatches	0;
			Indels	36;
			Gaps	1.
QY	8	GCAGCGCTGCGTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCATGCC	67	
Db	1	GCAGCGCTGCGTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCATGCC	60	
QY	68	GCGCGCTCCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCACACTACCGCGAGGTGCT	127	
Db	61	GCGCGCTCCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCACACTACCGCGAGGTGCT	120	
QY	128	GCGCGCTGCCACGTTGCTGCGGCGCGCTGGGGCCCCAGGGCTGCGCGTGTGCAGCGCGG	187	
Db	121	GCGCGCTGCCACGTTGCTGCGGCGCGCTGGGGCCCCAGGGCTGCGCGTGTGCAGCGCGG	180	
QY	188	GGACCCGGCGGCTTTCGCGCGCGCTGGTGGCCCAAGTGCCCTGGTGTGCGTGGCCCTGGGACGC	247	
Db	181	GGACCCGGCGGCTTTCGCGCGCGCTGGTGGCCCAAGTGCCCTGGTGTGCGTGGCCCTGGGACGC	240	
QY	248	ACGGCCGCCCCCGCGCGCCCTCTCTCCGCCAGGTGTCTGCTGAGGAGCTGGTGGC	307	
Db	241	ACGGCCGCCCCCGCGCGCCCTCTCTCCGCCAGGTGTCTGCTGAGGAGCTGGTGGC	300	
QY	308	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC	367	
Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC	360	
QY	368	GCTGTGAGCGGGGGCGCGGGGGCCCCCGAGGCCCTTACACCACACGCTGCCAGCTA	427	
Db	361	GCTGTGAGCGGGGGCGCGGGGGCCCCCGAGGCCCTTACACCACACGCTGCCAGCTA	420	
QY	428	CCTGCCCAACACGGTGAACCGACGACTGGGGGAGCGGGGCGTGGGGCTGCTGTCG	487	
Db	421	CCTGCCCAACACGGTGAACCGACGACTGGGGGAGCGGGGCGTGGGGCTGCTGTCG	480	
QY	488	CCGCGTGGGGCGAGACGTGCTGTTCACCTGCTGGACGCTGGCGCTCTTTGTGCTG	547	
Db	481	CCGCGTGGGGCGAGACGTGCTGTTCACCTGCTGGACGCTGGCGCTCTTTGTGCTG	540	
QY	548	GCGTCCACGCTGCGCTTACCAAGGTGTGGGGCGCGCGCTGTACCAAGCTTGGCGCTGCCAC	607	
Db	541	GCGTCCACGCTGCGCTTACCAAGGTGTGGGGCGCGCGCTGTACCAAGCTTGGCGCTGCCAC	600	
QY	608	TCAGGCGCGCGCGCGCCACACAGCTAGTGAACCCGGAAGGCGTGGGATGCGAAGCGGC	667	
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QY	668	CTGCAACCATATAGCCTCAGGGAGGCGCCCTGCGCCTGAGCCCGGGGTGCGAG	727
Db	661	CTGGAACCATATAGCCTCAGGGAGGCGCCCTGCGCCTGAGCCCGGGGTGCGAG	720
QY	728	GAGCGCGGGGGCGAGTGGCCAGCGGAAGTCTGCGCTTGCCCAAGAGGCCAGGGCTGGCGC	787
Db	721	GAGCGCGGGGGCGAGTGGCCAGCGGAAGTCTGCGCTTGCCCAAGAGGCCAGGGCTGGCGC	780
QY	788	TGCCCCCTGAGCCCGAGCGGAGCGCCCGTTGGCGAGGGGTCTGGGCCACACCCGGGCGAGGAC	847
Db	781	TGCCCCCTGAGCCCGAGCGGAGCGCCCGTTGGCGAGGGGTCTGGGCCACACCCGGGCGAGGAC	840
QY	848	GCGTGGACCGAGATGACCGGTGTGTCTGTGTGTGTACCTGGCCAGACCCGCGGAAGAAGC	907
Db	841	GCGTGGACCGAGATGACCGGTGTGTCTGTGTGTGTACCTGGCCAGACCCGCGGAAGAAGC	900
QY	908	CACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTCCACCCATCCGTGGCGCGCA	967
Db	901	CACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTCCACCCATCCGTGGCGCGCA	960
QY	968	GCACCAACGGGGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACAGCCTTGTC	1027
Db	961	GCACCAACGGGGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACAGCCTTGTC	1020
QY	1028	CCCGGTGTACGCCGAGACCAAGCACTTCTTACTCTCAGCGGACAAGAGACAGCTGCG	1087
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTTACTCTCAGCGGACAAGAGACAGCTGCG	1080
QY	1088	GCCCTCTCTCTACTACAGCTCTCTGAGGCCACAGCCTGACTGGCGCTCGAGAGCTCGTGA	1147
Db	1081	GCCCTCTCTCTACTACAGCTCTCTGAGGCCACAGCCTGACTGGCGCTCGAGAGCTCGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGCGCTGGATGCCAGGAGCTCCCGGACAGTGGCCCGCCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGCGCTGGATGCCAGGAGCTCCCGGACAGTGGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAAAATGGGCCCCCTGTCTTGAGAGTCTTGGAACCAACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAAATGGGCCCCCTGTCTTGAGAGTCTTGGAACCAACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCACAGC	1327
Db	1261	GTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCACAGC	1320
QY	1328	AGCGGCTGTCTGTGCCGGGAGAAAGCCCCAGAGGCTCTGTGGCGGCCCCCGAGAGGAGGA	1387
Db	1321	AGCGGCTGTCTGTGTGCCGGGAGAAAGCCCCAGAGGCTCTGTGGCGGCCCCCGAGAGGAGGA	1380
QY	1388	CACAGAACCCCGCTGCTGTGTGAGAGCTGCTCCGCCAGACAGACAGCCCTGGCAGGTGTA	1447
Db	1381	CACAGAACCCCGCTGCTGTGTGAGAGCTGCTCCGCCAGACAGACAGCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTCGTGCGGCGCTGCTGCGCCGGCTGGTGCCCCCAGGCGCTTGCGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGCGCTGCTGCGCCGGCTGGTGCCCCCAGGCGCTTGCGGCTCCAGGCA	1500
QY	1508	CAACGAAACGCCGCTCTCTCAGGAAACACCAAGAAGTTCACTCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAAACGCCGCTCTCTCAGGAAACACCAAGAAGTTCACTCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTTCGCTGACAGAGCTGACGTTGAAGATGAGCGTGGCGGACTGCGCTTGCGGCGAG	1627
Db	1561	GCTTCGCTGACAGAGCTGACGTTGAAGATGAGCGTGGCGGACTGCGCTTGCGGCGAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTTCGGGCGCAGACACCGTCTGGCGTGAGAGATCTTGGC	1687
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QY	1688	CAAGTTCTGCACTGGGCTGATGAGTGTGTACGTCGTGAGTCTCAGGTCTTTCTTTTA	1747
Db	1681	CAAGTTCTGCACTGGGCTGATGAGTGTGTGTACGTCGTGAGTCTCAGGTCTTTCTTTTA	1740
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[illegible]

Db 2821 GCCGGCCACGGCCCTATTCCTCGTGGCGCCCTGCTGCTGGATACCCGGAGCCCTGGAGGT 2880
QY 2852 GCAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCACCCTCAACCG 2911
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCACCCTCAACCG 2940
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Db 3301 GACTCGACACCGTGTACACCTACGTGCGCACTCTGCGGCTCAGTCTCAGACAGCCAGACGCA 3360
QY 3332 GCTGAGTCGGAAGCTCCCGGGAGCAGCCTGACTGCCCTGAGGCGCCAGCCAAACCCGCG 3391
Db 3361 GCTGAGTCGGAAGCTCCCGGGAGCAGCCTGACTGCCCTGAGGCGCCAGCCAAACCCGCG 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA 3451
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QY 3452 GAGCAGACACCAAGCAGCCCTGTACCGCCGGGCTCTACGTCCCAAGGAGGAGGGGGCGCC 3511
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QY 3512 CACACCCAGCCCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAATGTTTGGCCGAGGCCGTG 3571
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QY 3632 GAGTGTCCAGCACACCTGCGCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3691
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Db 3721 GGGCAGCTTTTCTCTACCAAGAGAGCCCGGCTTCCACTCCCCACATAGAATAGTCCATCC 3780
QY 3752 CCAGATTCGCCATTTGTCAACCCCTGCCCCCTGCCCCCTTGTGCTTCCACCCACCATCC 3811
Db 3781 CCAGATTCGCCATTTGTCAACCCCTGCCCCCTGCCCCCTTGTGCTTCCACCCACCATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAGGAGCCCTGAGAGCTCTGGAATTTGAGTGAACCAAGGTGTG 3871
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RESULT 6
US-09-721-456-1
: Sequence 1, Application US/09721456
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
: Lingner, Joachim
: Nakamura, Toru
: Chapman, Karen B.
: Morin, Gregg B.
: Harley, Calvin B.
: Andrews, William H.
: TITLE OF INVENTION: Human Telomerase Catalytic Subunit
: NUMBER OF SEQUENCES: 727
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/721,456
: FILING DATE: 22-Nov-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/974,549A
: FILING DATE: 19-Nov-1997
: APPLICATION NUMBER: US 08/724,643
: FILING DATE: 01-Oct-1996
: APPLICATION NUMBER: US 08/844,419
: FILING DATE: 18-Apr-1997
: APPLICATION NUMBER: US 08/846,017
: FILING DATE: 25-Apr-1997
: APPLICATION NUMBER: US 08/851,843
: FILING DATE: 06-May-1997
: APPLICATION NUMBER: US 08/854,050
: FILING DATE: 09-May-1997
: APPLICATION NUMBER: US 08/911,312
: FILING DATE: 14-Aug-1997
: APPLICATION NUMBER: US 08/912,951
: FILING DATE: 14-Aug-1997
: APPLICATION NUMBER: US 08/915,503
: FILING DATE: 14-Aug-1997
: APPLICATION NUMBER: WO PCT/US97/17618
: FILING DATE: 01-Oct-1997
: APPLICATION NUMBER: WO PCT/US97/17885
: FILING DATE: 01-Oct-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Apple, Randolph Ted
: REGISTRATION NUMBER: 36,429
: REFERENCE/DOCKET NUMBER: 015389-002610US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4015 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:

NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-721-456-1

Query Match 99.1%; Score 3969; DB 6; Length 4015;
Best Local Similarity 99.1%; Pred. No. 3.9e-111;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCGTGGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGC 127
Db 61 GCGCGCTCCCGCGTGGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGC 120
QY 128 GCGGTGGCCACGTTCGTGCGGCGCTGGGGCCCGAGGGCTGGCGGCTGGTGACAGCGCG 187
Db 121 GCGGTGGCCACGTTCGTGCGGCGCTGGGGCCCGAGGGCTGGCGGCTGGTGACAGCGCG 180
QY 188 GGACCCGGCGGCTTTCGCGCGCTGCTGGCCAGTGCCTGTGTGCTGCTGCTGCTGGAGCG 247
Db 181 GGACCCGGCGGCTTTCGCGCGCTGCTGGCCAGTGCCTGTGTGCTGCTGCTGCTGGAGCG 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCGCTTCCGCGAGGTGTCTGCGCTGAAGAGTGTGTGC 307
Db 241 ACGGCGCGCGCGCGCGCGCGCGCGCTTCCGCGAGGTGTCTGCGCTGAAGAGTGTGTGC 300
QY 308 CCGAGTGTCTGCAGAGGCTGTGCGAGCGCGCGCGCGAAGACGTGTGGCTTGGCTTGC 367
Db 301 CCGAGTGTCTGCAGAGGCTGTGCGAGCGCGCGCGCGAAGACGTGTGGCTTGGCTTGC 360
QY 368 GCTGTGGAGCGGCGCGCGCGCGCGCGCGCGCTTCAACACCGAGCGTGGCGAGCTA 427
Db 361 GCTGTGGAGCGGCGCGCGCGCGCGCGCGCGCTTCAACACCGAGCGTGGCGAGCTA 420
QY 428 CCTGCCCAACACGGTGAACCGACGACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGCG 487
Db 421 CCTGCCCAACACGGTGAACCGACGACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGCG 480
QY 488 CCGGTGGGCGACGAGTGTGTTCACCTGCTGGGACGCTGCGGCGCTTTTGTGTGTGT 547
Db 481 CCGGTGGGCGACGAGTGTGTTCACCTGCTGGGACGCTGCGGCGCTTTTGTGTGTGT 540
QY 548 GCGTCCAGCTGCGCCTACCAAGTGTGCGGGCGCGCTGTACCAAGCTGCGCGCTGCCAC 607
Db 541 GCGTCCAGCTGCGCCTACCAAGTGTGCGGGCGCGCTGTACCAAGCTGCGCGCTGCCAC 600
QY 608 TCAGGCGCGCGCGCGCGCGCGCGCGCTAGTGAACCCCGAAGCGCTTGGGATGCGAAGCG 667
Db 601 TCAGGCGCGCGCGCGCGCGCGCGCGCTAGTGAACCCCGAAGCGCTTGGGATGCGAAGCG 660
QY 668 CTGAACCATAGCGTCAAGGAGCGCGGGTCCCTGCGCTGCGAGCCCGGGTGGAG 727
Db 661 CTGAACCATAGCGTCAAGGAGCGCGGGTCCCTGCGCTGCGAGCCCGGGTGGAG 720
QY 728 GAGGCGCGGGGCGACTGCCAGCCGAAGTCTGCGCTTGGCCGAAGGCCAGGCGTGGCG 787
Db 721 GAGGCGCGGGGCGAGTGCACAGCGAAGTCTGCGCTTGGCCGAAGGCCAGGCGTGGCG 780
QY 788 TGCCCTGAGCGCGAGCGAGCGCGCTGGGCGAGGGTCTGGGCCACCGCGGAGAGC 847
Db 781 TGCCCTGAGCGCGAGCGAGCGCGCTGGGCGAGGGTCTGGGCCACCGCGGAGAGC 840
QY 848 GCGTGAACCGAGTGAACCGTGTCTGTGTGTGTACCTGTCCAGACCGCGCGAAGAGC 907
Db 841 GCGTGAACCGAGTGAACCGTGTCTGTGTGTGTACCTGTCCAGACCGCGCGAAGAGC 900

QY 908 CACCTCTTTGGAGGGTGGCGCTCTGTGGCACGGCGCACTCCCAACCATCCGTGGCGCGCA 967
Db 901 CACCTCTTTGGAGGGTGGCGCTCTGTGGCACGGCGCACTCCCAACCATCCGTGGCGCGCA 960
QY 968 GCACACAGCGGGCG 1027
Db 961 GCACACAGCGGGCG 1020
QY 1028 CCCGCTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGAGAGCAGTGC 1087
Db 1021 CCCGCTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGAGAGCAGTGC 1080
QY 1088 GCGCTCTCTCTACTACGCTCTGTGAGGCCCGAGCCTGACTGGCGCTCGGAGGCTGTGA 1147
Db 1081 GCGCTCTCTCTACTACGCTCTGTGAGGCCCGAGCCTGACTGGCGCTCGGAGGCTGTGA 1140
QY 1148 GACCATCTTCTGGGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1207
Db 1141 GACCATCTTCTGGGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1208 GCGCCAGCGCTACTGGCAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
Db 1201 GCGCCAGCGCTACTGGCAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GTGCGCGCTACGGGGTGTCTCTCAAGACGCACTGCGCGCGCTGCGAGCTGCGGTCAACCG 1327
Db 1261 GTGCGCGCTACGGGGTGTCTCTCAAGACGCACTGCGCGCGCTGCGAGCTGCGGTCAACCG 1320
QY 1328 AGCGGTGTCTGTGCGCGGAGAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
Db 1321 AGCGGTGTCTGTGCGCGGAGAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1388 CACAGACCGCGCGTGGCTGTGTGAGCTGTCTCGCGCGAGCACAGAGCGCGCGAGGTGA 1447
Db 1381 CACAGACCGCGCGTGGCTGTGTGAGCTGTCTCGCGCGAGCACAGAGCGCGCGAGGTGA 1440
QY 1448 GCGCTTGTGCGGGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1507
Db 1441 GCGCTTGTGCGGGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
QY 1508 CAAGAACCGCGCTTCTCTCAGGAACCAAGAAAGTTCATCTCCCTGGGGAACATGCCAA 1567
Db 1501 CAAGAACCGCGCTTCTCTCAGGAACCAAGAAAGTTCATCTCCCTGGGGAACATGCCAA 1560
QY 1568 GCTTCTGCTGCAAGAGCTGACGTGAAGATGAGGCTGCGGAGCTGCGCTTGTCTTTA 1627
Db 1561 GCTTCTGCTGCAAGAGCTGACGTGAAGATGAGGCTGCGGAGCTGCGCTTGTCTTTA 1620
QY 1628 GAGCCAGGGGTTGGCTGTGTTCGCGCGCGAGAGCACCGTGTGAGAGATCTTGGC 1687
Db 1621 GAGCCAGGGGTTGGCTGTGTTCGCGCGCGAGAGCACCGTGTGAGAGATCTTGGC 1680
QY 1688 CAAGTTCGCACTGGCTGATGAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTCTTTA 1747
Db 1681 CAAGTTCGCACTGGCTGATGAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTCTTTA 1740
QY 1748 TGTCAAGGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTGAG 1807
Db 1741 TGTCAAGGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTGAG 1800
QY 1808 CAAGTTCGAAGCATTTGAATCAGACAGCACTTGAAGAGGGTCAAGTGTGCGGAGCTGTC 1867
Db 1801 CAAGTTCGAAGCATTTGAATCAGACAGCACTTGAAGAGGGTCAAGTGTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAAGGAGCATGCGGGAAGCCAGGCGCGCGCTGTGAGCTGCCAGACTCG 1927
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QY 1928 CTTCAATCCCAAGCCTGACGGGGCTGGCGCGCGATTTGAACATGAGTACGTGCTGGAGC 1987
Db 1921 CTTCAATCCCAAGCCTGACGGGGCTGGCGCGCGATTTGAACATGAGTACGTGCTGGAGC 1980
QY 1988 CAGAACGTTCCGACAGAAAGAGGGCGAGCGCTCACCTCGAAGGGTGAAGGCACTGTT 2047

Db 1981 CAGAACGTTCCGACAGAGAAAAGAGGCGGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040
QY 2048 CAGCGTGTCAACTAGAGAGCGGGCGGCGCCCGGCTCTGGGCGCTCTGTGTGG 2107
Db 2041 CAGCGTGTCAACTAGAGAGCGGGCGGCGCCCGGCTCTGGGCGCTCTGTGTGG 2100
QY 2108 CCTGACGATATCCACAGGGCGCTGGCGCACTTGTGTGTGTGTGGGGCCAGAGACC 2167
Db 2101 CCTGACGATATCCACAGGGCGCTGGCGCACTTGTGTGTGTGTGGGGCCAGAGACC 2160
QY 2168 GCGGCTGTAGCTGT-----CATCCCCCA 2191
Db 2161 GCGGCTGTAGCTGTACTTGTCAAGGTGATGTGACGGGCGCTGACGACACCATCCCCCA 2220
QY 2192 GGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCTGCG 2251
Db 2221 GGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCTGCG 2280
QY 2252 TCGGTATGCGGTGTGCAGAGGCGCGCATGGGACGTCGCAAGCCTTCAAGAGCCA 2311
Db 2281 TCGGTATGCGGTGTGCAGAGGCGCGCATGGGACGTCGCAAGCCTTCAAGAGCCA 2340
QY 2312 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGCTCACTGACAGA 2371
Db 2341 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGCTCACTGACAGA 2400
QY 2372 GACCAAGCCGCTGAGGAGTCCGTCATCGAGCAGAGCTCCCTGAATGAGGCCAG 2431
Db 2401 GACCAAGCCGCTGAGGAGTCCGTCATCGAGCAGAGCTCCCTGAATGAGGCCAG 2460
QY 2432 CAGTGGCTCTTCGACGCTTCCCTACGCTTCATGTGCCACACCGCGTGCGCATGAGGG 2491
Db 2461 CAGTGGCTCTTCGACGCTTCCCTACGCTTCATGTGCCACACCGCGTGCGCATGAGGG 2520
QY 2492 CAAGTCTTACGTCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCCACAGCTGCTGTG 2551
Db 2521 CAAGTCTTACGTCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCCACAGCTGCTGTG 2580
QY 2552 CAGCGTGTCTACGCGCAGATGAGAACAAAGCTGTTGCGGGATTCGCGGGAGCGGCT 2611
Db 2581 CAGCGTGTCTACGCGCAGATGAGAACAAAGCTGTTGCGGGATTCGCGGGAGCGGCT 2640
QY 2612 GCTCTGCGTTTGGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGCGAAAC 2671
Db 2641 GCTCTGCGTTTGGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGCGAAAC 2700
QY 2672 CTTCCTCAGAACCTTGTCCGAGGTGTCCTGAGTATGGCTGCGTGTGAACCTTGGCGAA 2731
Db 2701 CTTCCTCAGAACCTTGTCCGAGGTGTCCTGAGTATGGCTGCGTGTGAACCTTGGCGAA 2760
QY 2732 GACAGTGTGAACCTTCCCTGTAGAACGAGGCCCTGGGTGGCAGGCTTTGTTAGAT 2791
Db 2761 GACAGTGTGAACCTTCCCTGTAGAACGAGGCCCTGGGTGGCAGGCTTTGTTAGAT 2820
QY 2792 GCGGCGCCACGCGCTATTTCCCTGTGCGGCGCTGCTGTGATACCGGAGACCTGAGGT 2851
Db 2821 GCGGCGCCACGCGCTATTTCCCTGTGCGGCGCTGCTGTGATACCGGAGACCTGAGGT 2880
QY 2852 GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2911
Db 2881 GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGAGGAGACATGCGCAAACTCTTTGGGCTTGGCGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGAGGAGACATGCGCAAACTCTTTGGGCTTGGCGCTGAAGTG 3000
QY 2972 TCACAGCTGTTTCTGATTTGACAGTGAACAGCCTCCAGAGCGGTGACCAACATCTA 3031
Db 3001 TCACAGCTGTTTCTGATTTGACAGTGAACAGCCTCCAGAGCGGTGACCAACATCTA 3060
QY 3032 CAAGATCTCTGCTGACAGGCGTACAGGTTTCAAGCATGTGTGCTCAGCTCCCATTTCA 3091

Db 3061 CAAGATCTCTGCTGCTGACAGGCGTACAGGTTTACGCATGTGTGCTCAGCTCCCATTTCA 3120
QY 3092 TCACAGCTTTTGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGGCGCTCCCT 3151
Db 3121 TCACAGCTTTTGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGGCGCTCCCT 3180
QY 3152 CTGCTACTCATCTTGAAGAACCCAGAGGATGTGCTGGGGCCAAAGGCGCGCG 3211
Db 3181 CTGCTACTCATCTTGAAGAACCCAGAGGATGTGCTGGGGCCAAAGGCGCGCG 3240
QY 3212 CGGCGCTGCGCTCCGAGGCGGTGCTGCTGTGCGCACCAAGCATTTCTGCTCAAGCT 3271
Db 3241 CGGCGCTGCGCTCCGAGGCGGTGCTGCTGTGCGCACCAAGCATTTCTGCTCAAGCT 3300
QY 3272 GACTGACACCGTGTACACCTACGTGCGCACTCTGGGGTCACTCAGAGACAGCCAGCGCA 3331
Db 3301 GACTGACACCGTGTACACCTACGTGCGCACTCTGGGGTCACTCAGAGACAGCCAGCGCA 3360
QY 3332 GCTGAGTCGAGACTCCCGGGGACGACGCTGACTGCGCTGAGGCGCGCAGCCACCGCGC 3391
Db 3361 GCTGAGTCGAGACTCCCGGGGACGACGCTGACTGCGCTGAGGCGCGCAGCCACCGCGC 3420
QY 3392 ACTGCGCTCAGACTTCAAGACCATCTGAGACTGATGGCCACCCGCGCAGCCAGCGCGA 3451
Db 3421 ACTGCGCTCAGACTTCAAGACCATCTGAGACTGATGGCCACCCGCGCAGCCAGCGCGA 3480
QY 3452 GAGCAGACACGACGCGCTGTACGCGCGGCTCTACGTCCACGAGGAGGAGGCGCGCC 3511
Db 3481 GAGCAGACACGACGCGCTGTACGCGCGGCTCTACGTCCACGAGGAGGAGGCGCGCC 3540
QY 3512 CACACCCAGGCGCGCACCGCTGGAGACTGAGCGCTGAGTGAAGTGTGGCGGAGGCTG 3571
Db 3541 CACACCCAGGCGCGCACCGCTGGAGACTGAGCGCTGAGTGAAGTGTGGCGGAGGCTG 3600
QY 3572 CATGTCGCGTGAAGGCTGAGTGTCCGCGTGAAGGCTGAGCGAGTGTCCAGCCAGGCGCT 3631
Db 3601 CATGTCGCGTGAAGGCTGAGTGTCCGCGTGAAGGCTGAGCGAGTGTCCAGCCAGGCGCT 3660
QY 3632 GAGTGTCCAGCACACTGCGGCTTTCACCTTCCACAGGCTGCGGCTCGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGCACACTGCGGCTTTCACCTTCCACAGGCTGCGGCTCGGCTCCACCCCA 3720
QY 3692 GGGCGAGCTTTTCTTCCACAGAGGCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3751
Db 3721 GGGCGAGCTTTTCTTCCACAGAGGCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTCGCAATGTTTCAACCCCTGCGCTGCGCTCTTGTGCTTCCACCCACCATCC 3811
Db 3781 CCAGATTCGCAATGTTTCAACCCCTGCGCTGCGCTCTTGTGCTTCCACCCACCATCC 3840
QY 3812 AGGTGAGACCCCTGAGAGGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3871
Db 3841 AGGTGAGACCCCTGAGAGGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGCGGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAATTTGGGGG 3931
Db 3901 CCCTGTACACAGCGGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAATTTGGGGG 3960
QY 3932 GAGGTGCTGTGGAGTAAATATGATATGAGTTTTCAGTTTGAAGAAAAA 3986
Db 3961 GAGGTGCTGTGGAGTAAATATGATATGAGTTTTCAGTTTGAAGAAAAA 4015

RESULT 7
US-09-949-016-455
; Sequence 455, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 455
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-455

Query Match 99.1%; Score 3969; DB 7; Length 4015;
Best Local Similarity 99.1%; Pred. No. 3.9e-111;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCGCCGACCCCGCGATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCGCCGACCCCGCGATGCC 60
QY 68 GCGCGTCCCCGCTGCGAGCCGTGGCTCCCTGCTGCGACCACTACCGGAGGTGCT 127
Db 61 GCGCGTCCCCGCTGCGAGCCGTGGCTCCCTGCTGCGACCACTACCGGAGGTGCT 120
QY 128 GCCGCTGCGCACGTTCTGCGGCGCTGGGGCCCAAGGCTGGCGGCTGTGACGCGG 187
Db 121 GCCGCTGCGCACGTTCTGCGGCGCTGGGGCCCAAGGCTGGCGGCTGTGACGCGG 180
QY 188 GGACCCGCGGCTTTCGCGCGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 247
Db 181 GGACCCGCGGCTTTCGCGCGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 248 ACGGCG 307
Db 241 ACGGCG 300
QY 308 CCGAGTGTGTCAGAGGCTGTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
Db 301 CCGAGTGTGTCAGAGGCTGTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 368 GCTGCTGACGGGCG 427
Db 361 GCTGCTGACGGGCG 420
QY 428 CCTGCCCAACAGGTGACGCGACGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 487
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QY 488 CCGCGTGGCGGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 547
Db 481 CCGCGTGGCGGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 548 GCGTCCCACTGCGCTTACCAAGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 607
Db 541 GCGTCCCACTGCGCTTACCAAGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGGAACCATAGCGTCAGGGGAGGCGCGGCGTCCCTGGCGCTGCGACGCCCGG 727
Db 661 CTGGAACCATAGCGTCAGGGGAGGCGCGGCGTCCCTGGCGCTGCGACGCCCGG 720
QY 728 GAGGCGCGGCGGCGAGTGCACAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGG 787
Db 721 GAGGCGCGGCGGCGAGTGCACAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGG 780
QY 788 TGCCCTGAGCCGAGGCGGACGCCGTTGGGCGAGGGTCTGGGCCACCCGCGGAG 847
Db 781 TGCCCTGAGCCGAGGCGGACGCCGTTGGGCGAGGGTCTGGGCCACCCGCGGAG 840

QY 848 GCGTGGACCGAGTGACCGGTGTTCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 907
Db 841 GCGTGGACCGAGTGACCGGTGTTCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 908 CACCTCTTTGAGGGGTGCGCTCTCTGCGACGCGGCGGCGGCGGCGGCGGCGGCG 967
Db 901 CACCTCTTTGAGGGGTGCGCTCTCTGCGACGCGGCGGCGGCGGCGGCGGCGGCG 960
QY 968 GCACACGCGGCG 1027
Db 961 GCACACGCGGCG 1020
QY 1028 CCGGCTGACGCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGAGAGCTGCG 1087
Db 1021 CCGGCTGACGCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGAGAGCTGCG 1080
QY 1088 GCGCTCTCTCTACTGAGCTCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1147
Db 1081 GCGCTCTCTCTACTGAGCTCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
QY 1148 GACCATCTTTCTGGGGTTCAGGGCCCTGATGCGGAGGACTCCCGGAGGTTGCCCGGCT 1207
Db 1141 GACCATCTTTCTGGGGTTCAGGGCCCTGATGCGGAGGACTCCCGGAGGTTGCCCGGCT 1200
QY 1208 GCGCCAGCGCTACTGGCAAAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1267
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Db 1321 AGCGGCTGTCTGTGCGCGGAGGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1380
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Db 1381 CACAGACCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1448 CGGCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1507
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QY 1508 CAACGAACGCGGCTTCTCTAGGAACACCAAGATTCTCTCTGGGGAAGCATGCCAA 1567
Db 1501 CAACGAACGCGGCTTCTCTAGGAACACCAAGATTCTCTCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCTGACAGAGCTGAGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGCAG 1627
Db 1561 GCTCTGCTGACAGAGCTGAGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGCAG 1620
QY 1628 GAGCCCAAGGGTGGCTGTGTTCGCGCGGCGGAGACCGCTGCGTGAAGAGATCTGGC 1687
Db 1621 GAGCCCAAGGGTGGCTGTGTTCGCGCGGCGGAGACCGCTGCGTGAAGAGATCTGGC 1680
QY 1688 CAAGTCTCTGCACTGGCTGATGATGATGATGATGATGATGATGATGATGATG 1747
Db 1681 CAAGTCTCTGCACTGGCTGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 1748 TGTCAAGGAGACACGTTTCAAAAGAACAGGCTTTTCTACCGAAGAGTGTCTGAG 1807
Db 1741 TGTCAAGGAGACACGTTTCAAAAGAACAGGCTTTTCTACCGAAGAGTGTCTGAG 1800
QY 1808 CAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGAAGTGGCGGAGCTGTC 1867
Db 1801 CAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGAAGTGGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAGGACGATCGGGAAGCCAGGCGCGCGCTGCTGACGTCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTCAGGACGATCGGGAAGCCAGGCGCGCGCTGCTGACGTCAGACTCCG 1920

QY 1928 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGACTACGTCTGGAGC 1987
 Db 1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGACTACGTCTGGAGC 1980
 QY 1988 CAGAACGTTCCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCATGTT 2047
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 QY 2048 CAGCGTGTCAACTACGAGCGGGCGCGGCCCTCTGGGCGCTCTGTCTGGG 2107
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 QY 2108 CCTGACGATATCCACAGGGCCTGGCGACCTTCGTCTGTCTGTGGGCGGAGACCC 2167
 Db 2101 CCTGACGATATCCACAGGGCCTGGCGACCTTCGTCTGTCTGTGGGCGGAGACCC 2160
 QY 2168 GCCGCTGAGCTGA-----CATCCCCCA 2191
 Db 2161 GCCGCTGAGCTGA-----CATCCCCCA 2220
 QY 2192 GGACAGGCTACCGAGGCTCATCGCCAGCATCATCAAAACCCAGAACACGTTACGTCGG 2251
 Db 2221 GGACAGGCTACCGAGGCTCATCGCCAGCATCATCAAAACCCAGAACACGTTACGTCGG 2280
 QY 2252 TCGGTATGCCGTGTCAGAAAGGCCCGCCATGGGACGTCCGCAAGGCCCTTCAAGAGCCA 2311
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 QY 2312 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTCACTGACAGGA 2371
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 QY 2552 CAGCCTGTGCTACGGCGACATGAGAACAGCGCTTTCGGGGATTGGCGGAGCGGGCT 2611
 Db 2581 CAGCCTGTGCTACGGCGACATGAGAACAGCGCTTTCGGGGATTGGCGGAGCGGGCT 2640
 QY 2612 GCTCCTGCGTTGGTGATGATTTCTGTGTGACACCTCACCTCACCCAGCGGAAAC 2671
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 Db 3061 CAAGATCCTCCTGCTGACGGCGTACAGGTTTTCAGCATGTGTGCTGACGCTCCATTTCA 3120
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 QY 3152 CTGCTACTCCTCATCTGAAGAACCAAGAACGCGAGGATGTGCTGGGGGCCAAGCGCCGCG 3211
 Db 3181 CTGCTACTCCTCATCTGAAGAACCAAGAACGCGAGGATGTGCTGGGGGCCAAGCGCCGCG 3240
 QY 3212 CGGCGCTGCTGCTGCGAGGGCGGTGACAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT 3271
 Db 3241 CGGCGCTGCTGCTGCGAGGGCGGTGACAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT 3300
 QY 3272 GACTCGACACCGTGTCACTACGTGCGCACCTGCGGCTCACTCAGACAGCCAGACGCA 3331
 Db 3301 GACTCGACACCGTGTCACTACGTGCGCACCTGCGGCTCACTCAGACAGCCAGACGCA 3360
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 QY 3452 GAGCAGACACAGCAGCCCTGTACGCGCGGCTCTACGTCGCCAGGAGGAGGGCGGCC 3511
 Db 3481 GAGCAGACACAGCAGCCCTGTACGCGCGGCTCTACGTCGCCAGGAGGAGGGCGGCC 3540
 QY 3512 CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGTCGCGGAGGCGCTG 3571
 Db 3541 CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGTCGCGGAGGCGCTG 3600
 QY 3572 CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3631
 Db 3601 CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3660
 QY 3632 GAGTGTCCAGACACCTGCGCTTTCACCTTCCACACAGGCTGGCGCTCCACCCCA 3691
 Db 3661 GAGTGTCCAGACACCTGCGCTTTCACCTTCCACACAGGCTGGCGCTCCACCCCA 3720
 QY 3692 GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3751
 Db 3721 GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
 QY 3752 CCAGATTGCGCATTTTCACCCCTGCGCTGCTCTTGTGCTTCCACCCCAACCATCC 3811
 Db 3781 CCAGATTGCGCATTTTCACCCCTGCGCTGCTCTTGTGCTTCCACCCCAACCATCC 3840
 QY 3812 AGGTGAGACCTTGAGAGGAGCCCTGGGAGCTTGGAATTTGAGTGAACCAAGGTGTG 3871
 Db 3841 AGGTGAGACCTTGAGAGGAGCCCTGGGAGCTTGGAATTTGAGTGAACCAAGGTGTG 3900
 QY 3872 CCCTGTACACAGGCGAGGAGCCCTGACCTGTGAGTGGGCTCCCTGTGGGTCAAAATTGGGGG 3931
 Db 3901 CCCTGTACACAGGCGAGGAGCCCTGACCTGTGAGTGGGCTCCCTGTGGGTCAAAATTGGGGG 3960
 QY 3932 GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 3986
 Db 3961 GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGAAGAAAAA 4015

RESULT 8
 US-10-388-578-1
 ; Sequence 1, Application US/10388578
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation

APPLICANT: Stanton, Lawrence
APPLICANT: Ralph, Brandenberger
APPLICANT: Joseph, Gold D.
APPLICANT: John, Irving
APPLICANT: Mandalam, Ramkumar
APPLICANT: Mok, Michael
APPLICANT: Shelton, Dawne
TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of Hu
FILE REFERENCE: 135/001
CURRENT APPLICATION NUMBER: US/10/388,578
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Custom
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)..(3454)
OTHER INFORMATION:
US-10-388-578-1

Query Match 99.1%; Score 3969; DB 8; Length 4015;
Best Local Similarity 99.1%; Pred. No. 3.9e-111;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCGTCTGCTGCGACGTGGAGAGCCCTGGCCCGCCACACCCCGCGATGCC 67
Db 1 GCAGCGCTGCGTCTGCTGCGACGTGGAGAGCCCTGGCCCGCCACACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCGCTGCGAGCCGCTGCTGCTGCGACGCACTACCGCGAGTGTCT 127
Db 61 GCGCGCTCCCGCGCTGCGAGCCGCTGCTGCTGCGACGCACTACCGCGAGTGTCT 120
QY 128 GCGCGTGGCCACGTTCGTGCGGCGGCTGGGGCCCGACAGGCGTGGTGTGACAGCGCG 187
Db 121 GCGCGTGGCCACGTTCGTGCGGCGGCTGGGGCCCGACAGGCGTGGTGTGACAGCGCG 180
QY 188 GGACCCGCGCGCTTTCGCGCGCTGCTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 247
Db 181 GGACCCGCGCGCTTTCGCGCGCTGCTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 248 ACG 307
Db 241 ACG 300
QY 308 CGAGTCTGACAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db 301 CGAGTCTGACAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 368 GCTGCTGACAGGCG 427
Db 361 GCTGCTGACAGGCG 420
QY 428 CCG 487
Db 421 CCG 480
QY 488 CCGCGTGGCGGACGAGTGTGCTTCACTGCTGCGACGCTGCGCGCGCTTGTGCTGCTGT 547
Db 481 CCGCGTGGCGGACGAGTGTGCTTCACTGCTGCGACGCTGCGCGCGCTTGTGCTGCTGT 540
QY 548 GCGTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Db 541 GCGTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727

Db 661 CTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGCGCGCGCGCGAGTGGCCAGCGGAGTGTGCGGTTGCCAAGAGGCGCCAGCGGTGGCG 787
Db 721 GAGCGCGCGCGCGAGTGGCCAGCGGAGTGTGCGGTTGCCAAGAGGCGCCAGCGGTGGCG 780
QY 788 TGCCCCGTGACCGGAGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db 781 TGCCCCGTGACCGGAGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 848 GCGTGACCGAGTGACCGGTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db 841 GCGTGACCGAGTGACCGGTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTTGAGAGGTGGGCTCTGTGCGACGCGCGCACTCCACCCATCCGTGGCGCGCA 967
Db 901 CACCTCTTTGAGAGGTGGGCTCTGTGCGACGCGCGCACTCCACCCATCCGTGGCGCGCA 960
QY 968 GCACACGCGGCG 1027
Db 961 GCACACGCGGCG 1020
QY 1028 CCGCGGTGACCGCGGAGACCAAGCACTTCTCTACTCTCTAGCGGCGACCTGCGGCTGCGGA 1087
Db 1021 CCGCGGTGACCGCGGAGACCAAGCACTTCTCTACTCTCTAGCGGCGACCTGCGGCTGCGGA 1080
QY 1088 GCCCTCTCTCTACTAGCTCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1147
Db 1081 GCCCTCTCTCTACTAGCTCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1148 GACCATCTTTCTGCGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1207
Db 1141 GACCATCTTTCTGCGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 1208 GCGCGAGCGCTACTGGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
Db 1201 GCGCGAGCGCTACTGGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GTGCGCGCTACGCGGCGCTCTCAAGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCG 1327
Db 1261 GTGCGCGCTACGCGGCGCTCTCAAGAGCACTGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1328 AGCGGCTGTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
Db 1321 AGCGGCTGTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1388 CACAGACCGCGCTGCGCTGTGACAGTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1447
Db 1381 CACAGACCGCGCTGCGCTGTGACAGTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440
QY 1448 CGGCTTCTGCGCGGCG 1507
Db 1441 CGGCTTCTGCGCGGCG 1500
QY 1508 CAACGACCGCGCTTCTCAGGAACCAAGAGTCAATCTCCCTGGGGAAGCATGCGCAA 1567
Db 1501 CAACGACCGCGCTTCTCAGGAACCAAGAGTCAATCTCCCTGGGGAAGCATGCGCAA 1560
QY 1568 GCTCTGCTGACAGAGCTGACGTGGAACATGAGCGTGGGAGCTGCGCTTGGCTGGCGAG 1627
Db 1561 GCTCTGCTGACAGAGCTGACGTGGAACATGAGCGTGGGAGCTGCGCTTGGCTGGCGAG 1620
QY 1628 GAGCCAGGCGGTGCGTGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1687
Db 1621 GAGCCAGGCGGTGCGTGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1680
QY 1688 CAAGTCTCTGCACTGGCTGATGAGTGTGATGCTGCTGCAAGGTCTTCTTTT 1747
Db 1681 CAAGTCTCTGCACTGGCTGATGAGTGTGATGCTGCTGCAAGGTCTTCTTTT 1740
QY 1748 TGTCAAGGAGACCAAGTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTCTGGAG 1807

Db 1741 TGTCAGGAGAGACCAGCTTTCAAAAAGACAGGCTCTTTTCTACCGGGAAGAGTGTCTGGAG 1800
QY 1808 CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTTC 1867
Db 1801 CAAATTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTTC 1860
QY 1868 GGAAGCAGAGGTCAGGCGACATCGGGAAGCCAGGCCCCGCTGTGACGTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTCAGGCGACATCGGGAAGCCAGGCCCCGCTGTGACGTCCAGACTCCG 1920
QY 1928 CTTCAATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGAGACTACGTCTGGAGC 1987
Db 1921 CTTCAATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGAGACTACGTCTGGAGC 1980
QY 1988 CAGAACGTTCCGCGAGAGAAAAGAGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT 2047
Db 1981 CAGAACGTTCCGCGAGAGAAAAGAGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT 2040
QY 2048 CAGCGTGTCTCAACTACGAGCGGGCGCGGCCGCCCGGCTCTGTGGGCTGTGCTGGG 2107
Db 2041 CAGCGTGTCTCAACTACGAGCGGGCGCGGCCGCCCGGCTCTGTGGGCTGTGCTGGG 2100
QY 2108 CCTGGACGATATCCACAGGGGCTGCGGCACCTTCGTGCTGCTGTGCGGGCCAGAGACC 2167
Db 2101 CCTGGACGATATCCACAGGGGCTGCGGCACCTTCGTGCTGCTGTGCGGGCCAGAGACC 2160
QY 2168 GCCGCTGAGCTGTA-----CATCCCCA 2191
Db 2161 GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCA 2220
QY 2192 GGACAGGCTCACGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACGTAAGCTGCGTGC 2251
Db 2221 GGACAGGCTCACGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACGTAAGCTGCGTGC 2280
QY 2252 TCGGTATGCCGTGTCCAGAAAGGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCA 2311
Db 2281 TCGGTATGCCGTGTCCAGAAAGGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCA 2340
QY 2312 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2371
Db 2341 CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2400
QY 2372 GACCAAGCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCCTTGAATGAGGCCAG 2431
Db 2401 GACCAAGCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCCTTGAATGAGGCCAG 2460
QY 2432 CAGTGGCTCTTTCGACGTCTTCCATACGCTTCATGTGCCACACAGCCGTGCGCATGAGGG 2491
Db 2461 CAGTGGCTCTTTCGACGTCTTCCATACGCTTCATGTGCCACACAGCCGTGCGCATGAGGG 2520
QY 2492 CAACTCTACGTCAGTCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG 2551
Db 2521 CAACTCTACGTCAGTCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG 2580
QY 2552 CAGCCTGTGCTACGGCGACATGGAACAAGCTGTTTGGGGGATTCGGCGGAGCGGCT 2611
Db 2581 CAGCCTGTGCTACGGCGACATGGAACAAGCTGTTTGGGGGATTCGGCGGAGCGGCT 2640
QY 2612 GCTCCTGCGTTTGGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGGAAGAAC 2671
Db 2641 GCTCCTGCGTTTGGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGGAAGAAC 2700
QY 2672 CTTCTCAGGACCTTGGTCCGAGGTTCCTTGATATGGCTGCGTGTGAACCTTGGCGAA 2731
Db 2701 CTTCTCAGGACCTTGGTCCGAGGTTCCTTGATATGGCTGCGTGTGAACCTTGGCGAA 2760
QY 2732 GACAGTGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCAGCGCTTTGTTCAGAT 2791
Db 2761 GACAGTGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCAGCGCTTTGTTCAGAT 2820
QY 2792 GCCGCGCCACGGCCTATTCCCTGTGTGCGGCTGCTGTGATACCCGAGCCCTGAGGT 2851
Db 2821 GCCGCGCCACGGCCTATTCCCTGTGTGCGGCTGCTGTGATACCCGAGCCCTGAGGT 2880

QY 2852 GCAGAGGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCTTCAACCG 2911
Db 2881 GCAGAGGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGCTCTTGGCGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGCTCTTGGCGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGAGGCTGTGCACCAACATCTA 3031
Db 3001 TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGAGGCTGTGCACCAACATCTA 3060
QY 3032 CAAGATCCTCCTGCTGACGGCGTACAGGTTTCACGCATGTGTCTGACGCTCCATTTCA 3091
Db 3061 CAAGATCCTCCTGCTGACGGCGTACAGGTTTCACGCATGTGTCTGACGCTCCATTTCA 3120
QY 3092 TCAGCAAGTTTGAAAGAACCCACATTTTCTGCGCGTCAATCTTGACAGGCTCCCT 3151
Db 3121 TCAGCAAGTTTGAAAGAACCCACATTTTCTGCGCGTCAATCTTGACAGGCTCCCT 3180
QY 3152 CTGCTACTCCATCCTGAAAGCCAAAGACGAGGGATGTGCTGGGGCCAAAGGCGCGCG 3211
Db 3181 CTGCTACTCCATCCTGAAAGCCAAAGACGAGGATGTGCTGGGGCCAAAGGCGCGCG 3240
QY 3212 CGGCCCTCTGCCCTCCGAGGCCGTGAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT 3271
Db 3241 CGGCCCTCTGCCCTCCGAGGCCGTGAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGTGTCACTACGTGCGCACTCCTGGGGTCACTTCAGACAGCCAGACGCA 3331
Db 3301 GACTCGACACCGTGTCACTACGTGCGCACTCCTGGGGTCACTTCAGACAGCCAGACGCA 3360
QY 3332 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGGCGCGCAAGCCCGCGC 3391
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGGCGCGCAAGCCCGCGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTGGAAGTGAATGGCCACCCGCCACAGCCAGGCCGA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGGAAGTGAATGGCCACCCGCCACAGCCAGGCCGA 3480
QY 3452 GAGCAGACACGACGACCCCTGTACGCGCGGCTCTACGTCCAGGGAAGGAGGGGCGGCC 3511
Db 3481 GAGCAGACACGACGACCCCTGTACGCGCGGCTCTACGTCCAGGGAAGGAGGGGCGGCC 3540
QY 3512 CACACCCAGGCCCCGACCGCTGGGAGTCTGAGGCTGAGTGAATGTTTGGCCGAGGCTG 3571
Db 3541 CACACCCAGGCCCCGACCGCTGGGAGTCTGAGGCTGAGTGAATGTTTGGCCGAGGCTG 3600
QY 3572 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3631
Db 3601 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3660
QY 3632 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCACACAGGCTGGCGCTCGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCACACAGGCTGGCGCTCGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTCCCCACATFAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTCCCCACATFAGGAATAGTCCATCC 3780
QY 3752 CCAGATTCGCCATTGTTCAACCCCTGCGCCCTGCGCTCTTGCCTTCCACCCACCATCC 3811
Db 3781 CCAGATTCGCCATTGTTCAACCCCTGCGCCCTGCGCTCTTGCCTTCCACCCACCATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3871
Db 3841 AGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3872 CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAAAATTGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAAAATTGGGG 3960

QY	3932	GAGGTGCTGTGGAGTAATAATGATGATATATGAGTTTTCAGTTTGTGA	3986
Db	3961	GAGGTGCTGTGGAGTAATAATGATGATATATGAGTTTTCAGTTTGTGA	4015
RESULT 9			
US-10-389-431-1			
: Sequence 1, Application US/10389431			
: GENERAL INFORMATION:			
: APPLICANT: Geron Corporation			
: APPLICANT: Stanton, Lawrence			
: APPLICANT: Ralph, Brandenberger			
: APPLICANT: Joseph, Gold D.			
: APPLICANT: John, Irving			
: APPLICANT: Mandalam, Ramkumar			
: APPLICANT: Mok, Michael			
: TITLE OF INVENTION: A Marker System for Preparing and Characterizing High-Quality Hum			
: TITLE OF INVENTION: Embryonic Stem Cells			
: FILE REFERENCE: 135/002			
: CURRENT APPLICATION NUMBER: US/10/389,431			
: CURRENT FILING DATE: 2003-03-13			
: NUMBER OF SEQ ID NOS: 100			
: SOFTWARE: PatentIn version 3.1			
: SEQ ID NO 1			
: LENGTH: 4015			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (56)..(3454)			
: OTHER INFORMATION:			
US-10-389-431-1			
Query Match 99.1%; Score 3969; DB 8; Length 4015;			
Best Local Similarity 99.1%; Pred. No. 3.9e-111;			
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;			
QY	8	GCAGCGCTGCTGCTGCTGCGACATGGGAAGCCCTGGCCCGCCACCCCGCGATGCC	67
Db	1	GCAGCGCTGCTGCTGCTGCGACATGGGAAGCCCTGGCCCGCCACCCCGCGATGCC	60
QY	68	GCGCGCTCCCGGCTGCCGAGCCGTGGCTCCCTGCTGCGACGCACTACCCGAGGTGCT	127
Db	61	GCGCGCTCCCGGCTGCCGAGCCGTGGCTCCCTGCTGCGACGCACTACCCGAGGTGCT	120
QY	128	GCCGCTGGCCACGTGCTGCGCGCCCTGGGGCCCGCAGGGCTGGCGGCTGTGACGGCGG	187
Db	121	GCCGCTGGCCACGTGCTGCGCGCCCTGGGGCCCGCAGGGCTGGCGGCTGTGACGGCGG	180
QY	188	GGACCCGGCGGCTTTCGGCGGCTGGTGGCCCACTGCTGTGTGCGTGGCCCTGGAGCGC	247
Db	181	GGACCCGGCGGCTTTCGGCGGCTGGTGGCCCACTGCTGTGTGCGTGGCCCTGGAGCGC	240
QY	248	ACGGCCGCCCCCGCGCCCTCTCCGACAGTGTCTGCTGAGGAGCTGTGGC	307
Db	241	ACGGCCGCCCCCGCGCCCTCTCTCCGACAGTGTCTGCTGAGGAGCTGTGGC	300
QY	308	CCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGCAAGACGTGCTGGCTTGGCTTGGC	367
Db	301	CCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGCAAGACGTGCTGGCTTGGCTTGGC	360
QY	368	GCTGCTGACGGGGCGCGGGGGCCCCCGAGGCTTACCAACAGCGTGGCGAGCTA	427
Db	361	GCTGCTGACGGGGCGCGGGGGCCCCCGAGGCTTACCAACAGCGTGGCGAGCTA	420
QY	428	CCTGCCCAACAGGCTACCGACGCACTGCGGGGAGCGGGGCTGGGGCTGTGCTGCG	487
Db	421	CCTGCCCAACAGGCTACCGACGCACTGCGGGGAGCGGGGCTGGGGCTGTGCTGCG	480
QY	488	CCGCGTGGCGACGAGCTGCTGTCACTGCTGACAGCTGCGCGCTTTGTGCTGCT	547
Db	481	CCGCGTGGCGACGAGCTGCTGTCACTGCTGACAGCTGCGCGCTTTGTGCTGCT	540

QY	548	GGCTCCAGCTGCGCCTACCAAGGTGTGGCGGCGCCGCGCTGTACAGCTCGCGCTGCCAC	607
Db	541	GGCTCCAGCTGCGCCTACCAAGGTGTGGCGGCGCCGCGCTGTACAGCTCGCGCTGCCAC	600
QY	608	TCAGGCGCGCGCGCGCGCCACACGCTAGTGGACCCCGAAGGCGTGTGGATGCCAAGGCG	667
Db	601	TCAGGCGCGCGCGCGCGCCACACGCTAGTGGACCCCGAAGGCGTGTGGATGCCAAGGCG	660
QY	668	CTGGAACCAATAGCGTCAGGGAGGCGCGGGTCCCTGTGGGCTGCCAGCCCGGGTGGAG	727
Db	661	CTGGAACCAATAGCGTCAGGGAGGCGCGGGTCCCTGTGGGCTGCCAGCCCGGGTGGAG	720
QY	728	GAGCGCGCGGGCGAGTGCACAGCCGAAGTCTGCCGTGGCCCAAGAGGCCACAGCGTGGCC	787
Db	721	GAGCGCGCGGGCGAGTGCACAGCCGAAGTCTGCCGTGGCCCAAGAGGCCACAGCGTGGCC	780
QY	788	TGCCCCGTGAGCCGAGCGGACCGCCCGTTGGGCAAGGGTCTGTGGCCACCCGGGCAAGAC	847
Db	781	TGCCCCGTGAGCCGAGCGGACCGCCCGTTGGGCAAGGGTCTGTGGCCACCCGGGCAAGAC	840
QY	848	GCGTGGACCGAGTACCGGTGTTTCTGTGTGGTGTGTCACTTGCACAGACCCCGCGAAGAGC	907
Db	841	GCGTGGACCGAGTACCGGTGTTTCTGTGTGGTGTGTCACTTGCACAGACCCCGCGAAGAGC	900
QY	908	CACCTCTTTGGAGGGTGGCGTCTCTGTGGACGCGCCACTCCACCCATCCGTGGGCGCGCA	967
Db	901	CACCTCTTTGGAGGGTGGCGTCTCTGTGGACGCGCCACTCCACCCATCCGTGGGCGCGCA	960
QY	968	GCACCACGGGGCGCGCCCATTCACATCGCGGGCCACACAGTCCCTGGGACACGCTTGTCC	1027
Db	961	GCACCACGGGGCGCGCCCATTCACATCGCGGGCCACACAGTCCCTGGGACACGCTTGTCC	1020
QY	1028	CCCGGTGTACCGCGAGACCAAGCACATTTCCTACTCTCAGGGCGACAGAGAGAGCTGGC	1087
Db	1021	CCCGGTGTACCGCGAGACCAAGCACATTTCCTACTCTCAGGGCGACAGAGAGAGCTGGC	1080
QY	1088	GCCCTCTTCTCTACTCAAGCTCTGTAGGCGCCAGCCTGACTGGCGCTCGAGGCTGTGGA	1147
Db	1081	GCCCTCTTCTCTACTCAAGCTCTGTAGGCGCCAGCCTGACTGGCGCTCGAGGCTGTGGA	1140
QY	1148	GACCATCTTCTGTGGGTTCAGAGGCGCTGATGCGAGGACTCCCGCAGGTGCCCCCGCT	1207
Db	1141	GACCATCTTCTGTGGGTTCAGAGGCGCTGATGCGAGGACTCCCGCAGGTGCCCCCGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCGCCCTGTTTCTGGAAGCTGCTTGGGAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCGCCCTGTTTCTGGAAGCTGCTTGGGAACCAAGCGCA	1260
QY	1268	GTCGCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCACG	1327
Db	1261	GTCGCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCACG	1320
QY	1328	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCGAGGGCTGTGGCGGCGCCCGAGAGAGAGA	1387
Db	1321	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCGAGGGCTGTGGCGGCGCCCGAGAGAGAGA	1380
QY	1388	CACAGACCCCGCTGCGCTGTGACGTCTCCGCCAGCACAGACAGCCCTGGCAGGTGTA	1447
Db	1381	CACAGACCCCGCTGCGCTGTGACGTCTCCGCCAGCACAGACAGCCCTGGCAGGTGTA	1440
QY	1448	GCGCTTGTGCGGGCGCTGCTGCGCGCGCTGTGCCCCAGGCTCTTGGGGCTTCCAGGCA	1507
Db	1441	GCGCTTGTGCGGGCGCTGCTGCGCGCGCTGTGCCCCAGGCTCTTGGGGCTTCCAGGCA	1500
QY	1508	CAAGGAACGCGCTTCTCTAGGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGCCAA	1567
Db	1501	CAAGGAACGCGCTTCTCTAGGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGCCAA	1560
QY	1568	GCTCTGCTGACGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTGCTGACGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCACAGGGTGTGGCTGTCTTCCGGCGCGACAGCAACCGTCTGCGTGAGAGATCTCTGC	1687

Db	1621	GAGCCACGAGGGGTGGCTGTGTGTCCGGCCGACAGACACCCTCTGCGTGAGAGATTCCTGGC	1680
QY	1688	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCTCTCAGACTGCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCTCTCAGACTGCTTCTTTTA	1740
QY	1748	TGTCACGAGAGACCAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCACGAGAGACCAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTCGCAAGCATTTGGAATCAGACAGCATTGAAGAGGGTGCAGCTGCGGGAGCTGTC	1867
Db	1801	CAAGTTCGCAAGCATTTGGAATCAGACAGCATTGAAGAGGGTGCAGCTGCGGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGACGATCGGGGAAGCCAGGCCGCCCTGTGACGTCCAGACTCCG	1927
Db	1851	GGAAGCAGAGGTCAGGACGATCGGGGAAGCCAGGCCGCCCTGTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGAAATGAGTACGTCTGCGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGAAATGAGTACGTCTGCGGAGC	1980
QY	1988	CAGAACGTTCGCGACAGAAAAGAGGGCCGAGCGCTTCACCTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCGCGACAGAAAAGAGGGCCGAGCGCTTCACCTCGAGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGCTCACTACGACGCGGGCGCGGCCGCCCTCTGGGGCCTCTGTGCTGGG	2107
Db	2041	CAGCGTGCTCACTACGACGCGGGCGCGGCCGCCCTCTGGGGCCTCTGTGCTGGG	2100
QY	2108	CCTGGACGATATCCACAGGGCCCTGGCGCACCTTCGTCTGCTGCTGCGGGGCCAGGACCC	2167
Db	2101	CCTGGACGATATCCACAGGGCCCTGGCGCACCTTCGTCTGCTGCTGCGGGGCCAGGACCC	2160
QY	2168	GCCGCCCTGAGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTACGCGGGCGCGTACGACACCACTCCCCCA	2220
QY	2192	GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGG	2251
Db	2221	GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGG	2280
QY	2252	TGCGTATGCCGTGTGTCCAGAAAGCCGCCATGGCGCAGTCCGCAAGGCTTCAAGAGCCA	2311
Db	2281	TGCGTATGCCGTGTGTGTCCAGAAAGCCGCCATGGCGCAGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2312	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2371
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2400
QY	2372	GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGAGAGCTCCTCCCTGAATGAGGCCAG	2431
Db	2401	GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2432	CAGTGGCCTCTTGACGCTTCTCTACGCTTCATGTGCCACCAAGCCGTGCGCATCAGGGG	2491
Db	2461	CAGTGGCCTCTTGACGCTTCTCTACGCTTCATGTGCCACCAAGCCGTGCGCATCAGGGG	2520
QY	2492	CAAGTCTACGTCCAGTGGCCAGGGGATCCCGCAGAGGCTCCATCTCTCCACGCTGCTCTG	2551
Db	2521	CAAGTCTACGTCCAGTGGCCAGGGGATCCCGCAGAGGCTCCATCTCTCCACGCTGCTCTG	2580
QY	2552	CAGCCTGTGCTACGGGCGACATGGAGAACAAAGCTGTTTCCGGGGATTCCGGCGGACGGGCT	2611
Db	2581	CAGCCTGTGCTACGGGCGACATGGAGAACAAAGCTGTTTCCGGGGATTCCGGCGGACGGGCT	2640
QY	2612	GCTCCTGCGTTTGGTGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGCGAAAAAC	2671
Db	2641	GCTCCTGCGTTTGGTGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGCGAAAAAC	2700
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Db	2701	CTTCCTCAGGACCCTTGCTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAATCTGCGGAA	2760
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Db	2761	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
QY	2792	GCCGGCCACGGCCTATTTCCCTGTGTGGCGCTGCTGTGATACCCGAGCCCTGGAGGT	2851
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QY	2912	CGGCTTCAAGGCTGGGAGGAGACATGCGTCCGAACCTTTTGGGCTTGTGGGCTGAAGTG	2971
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QY	2972	TCACAGCCTGTTTCTTGATTTGCAGGTTGAACAGCCTCCAGACGGTGTGCACCAATCTA	3031
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QY	3032	CAAGATCTCCTCTGCTGCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCATTCA	3091
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QY	3092	TCAGCAAGTTTGAAGAACCACATTTTTCCTGCGCTCATCTCTGACACGGCCTCCCT	3151
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QY	3152	CTGCTACTCCATCTCTGAAAGCCAAAGACGACGAGGATGTCGTGGGGCCAAAGGCGCCGC	3211
Db	3181	CTGCTACTCCATCTCTGAAAGCCAAAGACGACGAGGATGTCGTGGGGCCAAAGGCGCCGC	3240
QY	3212	CGGCCCTTGCCCTCCGAGGCGCTGCAGTGGCTGTGCCAACCAAGCATTTCTGCTCAAGCT	3271
Db	3241	CGGCCCTTGCCCTCCGAGGCGCTGCAGTGGCTGTGCCAACCAAGCATTTCTGCTCAAGCT	3300
QY	3272	GACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCACGACGCA	3331
Db	3301	GACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCACGACGCA	3360
QY	3332	GCTGAGTGGAAAGCTCCCCGGGAGCAGCGCTGACTGCCCTGGAGGCCGACCAACCCGGC	3391
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QY	3392	ACTGCCCTCAGACTTCAAGACCATCTGAGCTGATGGCCACCCGCCACAGCCAGGCCGA	3451
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QY	3452	GAGCAGACACACGACGACCCCTGTACAGCCGGGCTCTACGTCCAGGAGGAGGAGGGCGGCC	3511
Db	3481	GAGCAGACACACGACGACCCCTGTACAGCCGGGCTCTACGTCCAGGAGGAGGAGGGCGGCC	3540
QY	3512	CACACCCAGGCCCCGACACCGCTGGGAGTGTGAGGCCCTGAGTGAAGTGTGGCCGAGGCCTG	3571
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QY	3572	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGGCCTGAGCGAGTGTCCAGCCAGGGCT	3631
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QY	3632	GAGTGTCCAGCACACCTGCGCTTTCACCTTCCACAGAGGCTGGCGCTGGCTCCACCCCA	3691
Db	3661	GAGTGTCCAGCACACCTGCGCTTTCACCTTCCACAGAGGCTGGCGCTGGCTCCACCCCA	3720
QY	3692	GGGCCAGCTTTCCTCACCAGGAGCCGGCTTCCACTCCCCACATAGGAATGTCCATCC	3751
Db	3721	GGGCCAGCTTTCCTCACCAGGAGCCGGCTTTCACCTCCCCACATAGGAATGTCCATCC	3780
QY	3752	CCAGATTGCGCAATTGTTACCCCCCTGCGCTGCGCTCTTGGCTTCCACCCCAACCATCC	3811
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[illegible]

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RESULT 10
US-10-208-243-1
; Sequence 1. Application US/10208243
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

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[illegible][illegible]

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Db 3721 GGGCCAGCTTTTCTCCACAGAGAGCCCGGCTCCACTCCCAACATAGAAATAGTCCATCC 3780
QY 3752 CCAGATTCCGCAATGTCTCACCCCTGCGCCCTGCTTGCCTTCCACCCCAACATCC 3811
Db 3781 CCAGATTCCGCAATGTCTCACCCCTGCGCCCTGCTTGCCTTCCACCCCAACATCC 3840
QY 3812 AGGTGAGAGACCCCTGAGAGAGACCCCTGGAGCTCTGGAAATTGGAGTGACCAAGGTGTG 3871
Db 3841 AGTGGAGAGCCCTGAGAGAGACCCCTGGAGCTCTGGAAATTGGAGTGACCAAGGTGTG 3900
QY 3872 CCTGTACACAGGCGAGGACCCCTGCACCTGTGATGGGGTCCCTGTGGTCAAAATTGGGGG 3931
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QY 3932 GAGGTGCTGTGGGAGTAAATATGATATGAGTTTTCAGTTTGAAGAAAAA 3986
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RESULT 11
US-10-325-810-1
; Sequence 1, Application US/10325810
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-Oct-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: WO PCT/US97/17885

;; FILING DATE: 01-Oct-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ausenhus, Scott L.
;; REGISTRATION NUMBER: 42,271
;; REFERENCE/DOCKET NUMBER: 015389-00262005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4015 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 56..3454
;; OTHER INFORMATION: /product= "hTERT"
;; /note= "human telomerase reverse
;; transcriptase (hTERT) catalytic protein
;; component"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-325-810-1

Query Match 99.1%; Score 3969; DB 9; Length 4015;
Best Local Similarity 99.1%; Pred. No. 3.9e-111;
Matches 3979; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTCTGCTGCGACAGTGGGAAGCCCTGGCCCGCCACACCCCGCATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGACAGTGGGAAGCCCTGGCCCGCCACACCCCGCATGCC 60

QY 68 GCGCGCTCCCGCTGCCGAGCCGCTGCTCCCTGCTGCGACGCCACTACCGGAGGTGCT 127
Db 61 GCGCGCTCCCGCTGCCGAGCCGCTGCTCCCTGCTGCGACGCCACTACCGGAGGTGCT 120

QY 128 GCCGCTGGCCAGTTCGTCGGCGGCGCCTGGGGGCCCCAGGGGCTGGCGGCTGTGACAGCCGG 187
Db 121 GCCGCTGGCCAGTTCGTCGGCGGCGCCTGGGGGCCCCAGGGGCTGGCGGCTGTGACAGCCGG 180

QY 188 GAGCCCGGGGCTTTCGCGCGCGCTGTGAGCCCAAGTGCCTGTGCTGTGCGCTGGAGCG 247
Db 181 GAGCCCGGGGCTTTCGCGCGCGCTGTGAGCCCAAGTGCCTGTGCTGTGCGCTGGAGCG 240

QY 248 ACGGCGCGCGCGCGCGCGCGCTTCCCTCCGCGAGTGTCTGCTGAAGAGCTGTGGC 307
Db 241 ACGGCGCGCGCGCGCGCGCGCTTCCCTCCGCGAGTGTCTGCTGAAGAGCTGTGGC 300

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QY 368 GCTGCTGAGCGGGGCG 427
Db 361 GCTGCTGAGCGGGGCG 420

QY 428 CCGCCCAACAGGTGACCGGACGCTGCGGGGAGCGGGGCGGGGCTGGGGGCTGCTGCTGCG 487
Db 421 CCGCCCAACAGGTGACCGGACGCTGCGGGGAGCGGGGCGGGGCGGGGCTGCTGCTGCG 480

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 Db 901 CACCTCTTTGAGAGGTGCGCTCTCTGCGACGCGCCACTCCACCCATCCGTGGGCCGCCA 960
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 Db 1021 CCGGCGTACGCGCGAGAACCAAGCACTTCTCTACTCTCAGGCGACAGAGCAGCTGCG 1080
 QY 1088 GCGCTCTTCTTACTACTAGCTCTCTGAGGCGCCAGCTGACTGGCGCTCGAGGCTCGTGA 1147
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 QY 1208 GCGCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGGAACACGCGCA 1267
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 Db 1201 GCGCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGGAACACGCGCA 1260
 QY 1268 GTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCGCTGCGAGTGGCTCACCCAGC 1327
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 Db 1261 GTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCGCTGCGAGTGGCTCACCCAGC 1320
 QY 1328 AGCGGCTGTCTGTGCCCCGGGAGAAAGCCCAAGGGCTCTGTGGCGGCCCGCGAGGAGGA 1387
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 Db 1321 AGCGGCTGTCTGTGCCCCGGGAGAAAGCCCAAGGGCTCTGTGGCGGCCCGCGAGGAGGA 1380
 QY 1388 CACAGACCCCGCTGCGCTGTGTCAGTGTCCGCCAGCACAGACGCGCTGCGAGGTGA 1447
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 Db 1381 CACAGACCCCGCTGCGCTGTGTCAGTGTCCGCCAGCACAGACGCGCTGCGAGGTGA 1440
 QY 1448 CGGCTTGTGCGGGGCTGCGCTGCGCGCGCTGTGCCAGGCGCTGTGGGCTCCAGGA 1507
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QY	2912	CGGCTTCAAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGGCGCTGAAGTG	2971	
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGGCGCTGAAGTG	3000	
QY	2972	TCACAGCCTGTTTCTGGAATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAATCTA	3031	
Db	3001	TCACAGCCTGTTTCTGGAATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAATCTA	3060	
QY	3032	CAAGATCCCTCTGCTGAGGCGTACAGGTTTTCACGCAATGTGTGCTGACCTCCATTTC	3091	
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QY	3152	CTGCTACTCCATCCTGAAAGCCAAAGAACGCAAGGATGTGCTGGGGCCCAAGGCGCGCG	3211	
Db	3181	CTGCTACTCCATCCTGAAAGCCAAAGAACGCAAGGATGTGCTGGGGCCCAAGGCGCGCG	3240	
QY	3212	CGGCGCTCTGCCCCCTCCGAGGCGGTGCACTGCTGTGCCAACCAAGCATTCCTGCTCAAGCT	3271	
Db	3241	CGGCGCTCTGCCCCCTCCGAGGCGGTGCACTGCTGTGCCAACCAAGCATTCCTGCTCAAGCT	3300	
QY	3272	GACTCGAACCCGTGTTCACCTACTGTCGCCACATCTCTGGGGTCACTCAGGACAGCCACGCA	3331	
Db	3301	GACTCGAACCCGTGTTCACCTACTGTCGCCACATCTCTGGGGTCACTCAGGACAGCCACGCA	3360	
QY	3332	GCTGAGTGGGAAGCTCCCGGGGAGCAGCGCTGACTGCCCCCTGAGAGCGCCAGCCAAACCCGCG	3391	
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QY	3632	GAGTGTCCAGCACACCTGCGCTTTCACATTCCACACAGGCTGGCGCTCGGCTCAACCCCA	3691	
Db	3661	GAGTGTCCAGCACACCTGCGCTTTCACATTCCACACAGGCTGGCGCTCGGCTCAACCCCA	3720	
QY	3692	GGGCGAGCTTTTCTTCACACAGAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3751	
Db	3721	GGGCGAGCTTTTCTTCACACAGAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780	
QY	3752	CCAGATTCCGCAATTGTTCACCCCTCGCCCTGCTCCCTTGTGCTTCCACCCCAACATCC	3811	
Db	3781	CCAGATTCCGCAATTGTTCACCCCTCGCCCTGCTCCCTTGTGCTTCCACCCCAACATCC	3840	
QY	3812	AGGTGAGACCCCTGAGAAAGAGCCCTGGAGCTCTGGGAAATTTGGAGTGAACCAAAAGTGTG	3871	
Db	3841	AGGTGAGACCCCTGAGAAAGAGCCCTGGAGCTCTGGGAAATTTGGAGTGAACCAAAAGTGTG	3900	
QY	3872	CCCTGTACACAGGCGAGACCTCTGACCTGATGGGGGTCCTGTGGGTCAAATTTGGGG	3931	
Db	3901	CCCTGTACACAGGCGAGACCTCTGACCTGATGGGGGTCCTGTGGGTCAAATTTGGGG	3960	

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      QY   3932 GAGCTGCTGTGGAGAGTAATAATACTGAATATATAGATTTTTTCAGTTTTTGAAAAAAA 3986
              |||||||
      Db    3961 GAGGTGCTGTGGGAGTAATAAATACTGAATATATAGATTTTTTCAGTTTTTGAAAAAAA 4015

RESULT 12
US-10-170-235-38656
; Sequence 38656, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
; FILE REFERENCE: C1001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 38656
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-38656

Query Match          99.1%; Score 3967.4; DB 8; Length 4015;
Best Local Similarity 99.1%; Pred. No. 4.4e-111;
Matches 3978; Conservative 0; Mismatches 1; Indels 36; Gaps 1;

      QY     8 GCACGCCTGCGTCTCTGCTGCGCACAGTGGGAAAGCCCTGGCCCCCGGCCAACCCCGCGATGCC 67
              |||||||
      Db     1 GCAGCGCTGCGTCTCTGCTGCGCACAGTGGGAAAGCCCTGGCCCCCGGCCAACCCCGCGATGCC 60

      QY    68 GCGCGCTCCCGCGCTGCGCAGCCGTGCGCTCCCTGCTGCGCAGCCACTACC CGSAGGTGCT 127
              |||||||
      Db     61 GCGCGCTCCCGCGCTGCGCAGCCGTGCGCTCCCTGCTGCGCAGCCACTACC CGSAGGTGCT 120

      QY    128 GCCGCTGGCCACGTTGCTGCGGCGCCTTGGGGCCCCCAGAGGCTGGCGGCTGTGACAGCGCG 187
              |||||||
      Db    121 GCGCGTGGCCACGTTGCTGCGGCGCCTTGGGGCCCCCAGAGGCTGGCGGCTGTGACAGCGCG 180

      QY    188 GGACCCGGCGGCTTCCGCGCGCTGTGTGCCCAGTGCCCTGTGTGCGCTGACCCTGGGACGC 247
              |||||||
      Db    181 GGACCCGGCGGCTTCCGCGCGCTGTGTGCCCAGTGCCCTGTGTGCGCTGACCCTGGGACGC 240

      QY    248 ACCGCGCGCCCCCGCGCGCCCTCTCTCCGCCAGGTGTCTGTGCTGAAGAGAGCTGTGGC 307
              |||||||
      Db    241 ACCGCGCGCCCCCGCGCGCCCTCTCTCCGCCAGGTGTCTGTGCTGAAGAGAGCTGTGGC 300

      QY    308 CCAGTGTCTGCAGAGGCTGTGTGCCAGCGCGCGCGAAGAAGCTGTGTGGCCTTGGCCTTCCG 367
              |||||||
      Db    301 CCAGTGTCTGCAGAGGCTGTGTGCCAGCGCGCGCGAAGAAGCTGTGTGGCCTTGGCCTTCCG 360

      QY    368 GCTGCTGGACGGGGGCCCCGCGGGGCCCCCGGAGGCCCTTCAACCAAGCGTGGCGACGTA 427
              |||||||
      Db    361 GCTGCTGGACGGGGGCCCCGCGGGGCCCCCGGAGGCCCTTCAACCAAGCGTGGCGACGTA 420

      QY    428 CCTGCCCAACAACGGTGAACCAACGCACTGGGGGGGAGCGGGGCGTGGGGGCTGCTGTGCG 487
              |||||||
      Db    421 CCTGCCCAACAACGGTGAACCAACGCACTGGGGGGGAGCGGGGCGTGGGGGCTGCTGTGCG 480

      QY    488 CCGCGTGGGCGACGACGTGTGTTCACTGCTGTCGCAAGCTGCGCGCTCTTTGTGTGTGT 547
              |||||||
      Db    481 CCGCGTGGGCGACGACGTGTGTTCACTGCTGTCGCAAGCTGCGCGCTCTTTGTGTGTGT 540

      QY    548 GCGTCCCAAGCTGCGCCTACCAAGGTGTGGGGGCGCGCGCTGTACCAAGCTGCGCGCTGCCAC 607
              |||||||
      Db    541 GCGTCCCAAGCTGCGCCTACCAAGGTGTGGGGGCGCGCGCTGTACCAAGCTGCGCGCTGCCAC 600

      QY    608 TCAGGCGCGGCGCGCGCGCAACAGCTAGTGGACCCCGAAGGCGTGTGGGATGCGAAGGGC 667
              |||||||
      Db    601 TCAGGCGCGGCGCGCGCGCAACAGCTAGTGGACCCCGAAGGCGTGTGGGATGCGAAGGGC 660

      QY    668 CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCTCCCTGGGCGCTGCGACGCCCGGGTGCAG 727
              |||||||

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Db	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCCCCTGGGCTTGCCAGCCCGGGTGGAG	720
QY	728	GAGCGCGGGGCGAGTGGCAGCCGAAGTCTGCCCCGTGGCCCAAGAGGCCAGCGTGGCGC	787
Db	721	GAGCGCGGGGCGAGTGGCAGCCGAAGTCTGCCCCGTGGCCCAAGAGGCCAGCGTGGCGC	780
QY	788	TGCCCCTGAGCCCGAGCGGACGCCCCGTTGGCAGGGGCTGGGCCCAACCCGGGCGAGGAC	847
Db	781	TGCCCCTGAGCCCGAGCGGACGCCCCGTTGGCAGGGGCTGGGCCCAACCCGGGCGAGGAC	840
QY	848	GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACTGCGACAGACCCCGCGAAGAACC	907
Db	841	GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACTGCGACAGACCCCGCGAAGAACC	900
QY	908	CACCTCTTTGGAGGGTGGCGCTCTCTGGCAGCGCGCCACTCCACCCATCCGTGGCGCGCA	967
Db	901	CACCTCTTTGGAGGGTGGCGCTCTCTGGCAGCGCGCCACTCCACCCATCCGTGGCGCGCA	960
QY	968	GCACCACGCGGGCCCCCATCCACATCGCGGGCCACCAGTCCCTGGGACACGCGTTGTCC	1027
Db	961	GCACCACGCGGGCCCCCATCCACATCGCGGGCCACCAGTCCCTGGGACACGCGTTGTCC	1020
QY	1028	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGCGCAGCAAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGCGCAGCAAGAGCAGCTGCG	1080
QY	1088	GCCCTCCTCTCTACTCTAGCTCTCTGAGGCCACGCTGACTGGCGCTCGAGGCTGTGGA	1147
Db	1081	GCCCTCCTCTCTACTCTAGCTCTCTGAGGCCACGCTGACTGGCGCTCGAGGCTGTGGA	1140
QY	1148	GACCATCTTCTGGGTGCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCGCCT	1207
Db	1141	GACCATCTTCTGGGTGCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGGCCCTGTTTCTGAGCTGCTTGGGAACCACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGGCCCTGTTTCTGAGCTGCTTGGGAACCACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCCCAGC	1327
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCCCAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGCGCGCCCCCGAGGAGGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGCGCGCCCCCGAGGAGGGA	1380
QY	1388	CACAGACCCCCGCTGCGCTGGTGACGTGCTCCGCCACAGCAGCAGCCCCCTGGCAGGTGTA	1447
Db	1381	CACAGACCCCCGCTGCGCTGGTGACGTGCTCCGCCACAGCAGCAGCCCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTCTGTGCGGGCTGCGCTGCGCGCGGCTGCTGCCCCCAGGGCCTTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCTGTGCGGGCTGCGCTGCGCGCGGCTGCTGCCCCCAGGGCCTTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGCGTGGCGCAG	1627
Db	1561	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGCGTGGCGCAG	1620
QY	1628	GAGCCACGAGGGTGGCTGTGTCCGGCCGACAGACACCTGTGCGTGAGAGATCTGCGC	1687
Db	1621	GAGCCACGAGGGTGGCTGTGTCCGGCCGACAGACACCTGTGCGTGAGAGATCTGCGC	1680
QY	1688	CAAGTCTCTGCACTGGCTGATGAGTGTGTACGTGTCGACCTGCTCAGGTCTTCTTTTA	1747
Db	1681	CAAGTCTCTGCACTGGCTGATGAGTGTGTGTACGTGTCGACCTGCTCAGGTCTTCTTTTA	1740
QY	1748	TGTCACGGAGACCACTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCACGGAGACCACTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800

OY	1808	CAAGTTGCCAAAGCATTTGGAATCAGACACACTTGAAGAGGGTGACGTCCGGGAGCTGTC	1867
Db	1801	CAAGTTGCCAAAGCATTTGGAATCAGACACACTTGAAGAGGGTGACGTCCGGGAGCTGTC	1860
OY	1868	GGAAGCAGAGGCTCAGGCAGCATCGGGAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGCTCAGGCAGCATCGGGAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1920
OY	1928	CTTCATCCCCAAGCCTGACGGGCTCGGCCGATTGTGAACATGAGTAAGTCTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTCGGCCGATTGTGAACATGAGTAAGTCTGGAGC	1980
OY	1988	CAGAAGCTTCCGCAGAGAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGCACTGTT	2047
Db	1981	CAGAAGCTTCCGCAGAGAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGCACTGTT	2040
OY	2048	CAGCGTGCTCAACTACGAGCGGGCGCGGCCGCCCTCCTGGGCGCTTGTGCTGGG	2107
Db	2041	CAGCGTGCTCAACTACGAGCGGGCGCGGCCGCCCTCCTGGGCGCTTGTGCTGGG	2100
OY	2108	CCTGGACGATATCCACAGGGGCTGGCGCACTTGTGCTGCGTGTGCGGGCCAGGACC	2167
Db	2101	CCTGGACGATATCCACAGGGGCTGGCGCACTTGTGCTGCGTGTGCGGGCCAGGACC	2160
OY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCTGAGCTGTACTTGTCAAGGTGATGTGACGGGCGGCTACGACACCATCCCCA	2220
OY	2192	GGACAGGCTCACGGAGGTGATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGG	2251
Db	2221	GGACAGGCTCACGGAGGTGATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGG	2280
OY	2252	TGCGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCCA	2311
Db	2281	TGCGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCCA	2340
OY	2312	CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGATTCGTGGCTCACCTGCAGGA	2371
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGATTCGTGGCTCACCTGCAGGA	2400
OY	2372	GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGAGACTCCTCCGTGAATGAGGCCAG	2431
Db	2401	GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGAGACTCCTCCGTGAATGAGGCCAG	2460
OY	2432	CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCAACACGCCCTGCGCATCAGGGG	2491
Db	2461	CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCAACACGCCCTGCGCATCAGGGG	2520
OY	2492	CAAGTCTTACGTCCAGTGCAGTGCAGGGGATCCCGCAGAGGCTCCATCCTCTCCACGCTGCTG	2551
Db	2521	CAAGTCTTACGTCCAGTGCAGGGGATCCCGCAGAGGCTCCATCCTCTCCACGCTGCTG	2580
OY	2552	CAGCCTGTGCTACGGCGACATGGAACAAGCTGTTTGCGGGGATTGGCGGGGACGGGCT	2611
Db	2581	CAGCCTGTGCTACGGCGACATGGAACAAGCTGTTTGCGGGGATTGGCGGGGACGGGCT	2640
OY	2612	GCTCCTGCGTTTGGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGCGAAAAC	2671
Db	2641	GCTCCTGCGTTTGGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGCGAAAAC	2700
OY	2672	CTTCCTCAGGACCCCTGTCGAGGTGTCCTTGAGTATGGCTGCGTGTGAACCTTGGCGAA	2731
Db	2701	CTTCCTCAGGACCCCTGTCGAGGTGTCCTTGAGTATGGCTGCGTGTGAACCTTGGCGAA	2760
OY	2732	GACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGGCTTTTGTTCAGAT	2820
OY	2792	GCGCGCCACGGCCTATTTCCCCTGGTGGCGCCCTGCTGCTGGATACCCGGACCTGGAGGT	2851
Db	2821	GCGCGCCACGGCCTATTTCCCCTGGTGGCGCCCTGCTGCTGGATACCCGGACCTGGAGGT	2880

QY 2852 GCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2911
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
QY 2912 CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 2971
Db 2941 CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
QY 2972 TCACAGCCTGTTCTGATTTGAGTTGACAGGTGAACAGCCTCCAGAGGTTGACCAACATCTA 3031
Db 3001 TCACAGCCTGTTCTGATTTGAGTTGACAGGTGAACAGCCTCCAGAGGTTGACCAACATCTA 3060
QY 3032 CAAGATCCTCTGCTGCAAGGCGTACAGGTTTTCAGGCATGTGTGCTGCAGCTCCCATTTCA 3091
Db 3061 CAAGATCCTCTGCTGCAAGGCGTACAGGTTTTCAGGCATGTGTGCTGCAGCTCCCATTTCA 3120
QY 3092 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTTGACAGGCGCTCCCT 3151
Db 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTTGACAGGCGCTCCCT 3180
QY 3152 CTGCTACTCCATCTCGAAGAACCAAGCAGCAGGATGTGCTGGGGGCCAAGGGCGCGC 3211
Db 3181 CTGCTACTCCATCTCGAAGAACCAAGCAGCAGGATGTGCTGGGGGCCAAGGGCGCGC 3240
QY 3212 CGGCCCTCTGCCCCCTCCGAGGCGCGTGCAGTGGGTGTCACCAAGCATTCCTGCTCAAGCT 3271
Db 3241 CGGCCCTCTGCCCCCTCCGAGGCGCGTGCAGTGGGTGTCACCAAGCATTCCTGCTCAAGCT 3300
QY 3272 GACTCGACACCGTGTGTCACCTACGTGCGCCTCTGCGGGTCACTCAGAGCAGCCAGACGCA 3331
Db 3301 GACTCGACACCGTGTGTCACCTACGTGCGCCTCTGCGGGTCACTCAGAGCAGCCAGACGCA 3360
QY 3332 GCTGAGTCGGAAGCTCCCGGGGAGACGCTGACTGCCCCCTGGAGGCCGACAGCCAAACCGGC 3391
Db 3361 GCTGAGTCGGAAGCTCCCGGGGAGACGCTGACTGCCCCCTGGAGGCCGACAGCCAAACCGGC 3420
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTTGACTGATGAGGCCACCCGCCACAGCCAGGCGCA 3451
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTTGACTGATGAGGCCACCCGCCACAGCCAGGCGCA 3480
QY 3452 GAGCAGACACGACGACGACCCCTGTACAGCCGCGGGCTCTACGTCCAGGAGGAGGGGGCGCC 3511
Db 3481 GAGCAGACACGACGACGACCCCTGTACAGCCGCGGGCTCTACGTCCAGGAGGAGGGGGCGCC 3540
QY 3512 CACACCCAGGCGCGCACCGCTGGGAGTCTGAGAGCCTGAGTGAAGTGTGGCGGAGGCGCTG 3571
Db 3541 CACACCCAGGCGCGCACCGCTGGGAGTCTGAGAGCCTGAGTGAAGTGTGGCGGAGGCGCTG 3600
QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGGAGTGTCCAGCCAAAGGCT 3631
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGGAGTGTCCAGCCAAAGGCT 3660
QY 3632 GAGTGTCCAGCACACCTGCGCTTCACTTCCACACAGGCTGGCGCTCGGGCTCCACCCCA 3691
Db 3661 GAGTGTCCAGCACACCTGCGCTTCACTTCCACACAGGCTGGCGCTCGGGCTCCACCCCA 3720
QY 3692 GGGCCAGCTTTTCTCTACCCAGGAGCGCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3751
Db 3721 GGGCCAGCTTTTCTCTACCCAGGAGCGCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780
QY 3752 CCAGATTGCGCCATTGTTCAACCCCTGCGCCCTGCGCTTGTGCTTCCACCCCCACCATCC 3811
Db 3781 CCAGATTGCGCCATTGTTCAACCCCTGCGCCCTGCGCTTGTGCTTCCACCCCCACCATCC 3840
QY 3812 AGGTGAGACCCCTGAGAAAGGACCCCTGGGAGCTCTGGGAATTTGAGTGAAGTGAACAAAGTGTG 3871
Db 3841 AGGTGAGACCCCTGAGAAAGGACCCCTGGGAGCTCTGGGAATTTGAGTGAAGTGAACAAAGTGTG 3900
QY 3872 CCCTGTACACAGGCGAGGACCCCTGACACTGATGGGGGTCCCTGTGGTCAAAATTTGGGG 3931
Db 3901 CCCTGTACACAGGCGAGGACCCCTGACACTGATGGGGGTCCCTGTGGTCAAAATTTGGGG 3960
QY 3932 GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAGAAAA 3986

Db 3961 GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAGAAAA 4015

RESULT 13
US-09-949-016-5841
; Sequence 5841, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5841
; LENGTH: 4016
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-5841

Query Match 98.7%; Score 3954.2; DB 7; Length 4016;
Best Local Similarity 99.0%; Pred. No. 1.1e-110;
Matches 3976; Conservative 0; Mismatches 3; Indels 37; Gaps 2;

QY 8 GCAGCGCTGCGTCTGCTGCGCACAGTGGGAAAGCCCTGGGCCCCCGCGCATGCC 67
Db 1 GCAGCGCTGCGTCTGCTGCGCACAGTGGGAAAGCCCTGGGCCCCCGCGCATGCC 60
QY 68 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGT 127
Db 61 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGT 120
QY 128 GCCGCTGGCCAGCTTCGTCGCGGCGGCTGGGGGCCCGCAGGGCTGGCGGCTGTGACGCGCG 187
Db 121 GCCGCTGGCCAGCTTCGTCGCGGCGGCTGGGGGCCCGCAGGGCTGGCGGCTGTGACGCGCG 180
QY 188 GGAACCCGCGGCTTTCGCGGCGCTGTGCGCCAGTGCCTGTGTGCGTGCCTGGGAGCG 247
Db 181 GGAACCCGCGGCTTTCGCGGCGCTGTGCGCCAGTGCCTGTGTGCGTGCCTGGGAGCG 240
QY 248 ACGGCGGCGGCGGCGGCGGCGGCTTCTTCCGCGCAGGTGTCTGCTGAAGAGCTGTGCG 307
Db 241 ACGGCGGCGGCGGCGGCGGCGGCTTCTTCCGCGCAGGTGTCTGCTGAAGAGCTGTGCG 300
QY 308 CCGAGTGTGAGAGGCTGTGCGAGCGGCGGCGGCGGAAGACGTGCTGGGCTTGGCGTGGC 367
Db 301 CCGAGTGTGAGAGGCTGTGCGAGCGGCGGCGGCGGAAGACGTGCTGGGCTTGGCGTGGC 360
QY 368 GCTGCTGAGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427
Db 361 GCTGCTGAGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 428 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGGAGCGGGGCGGCGGCGGCGGCGGCGG 487
Db 421 CCTGCCCAACACGGTGACCGACGCACTGCGGGGGGAGCGGGGCGGCGGCGGCGGCGGCGG 480
QY 488 CCGCGTGGGCGAGCAGTGTGCTGTTCACTTGCCTGCGGACGCTGCGCGCTCTTGTGCTGTG 547
Db 481 CCGCGTGGGCGAGCAGTGTGCTGTTCACTTGCCTGCGGACGCTGCGCGCTCTTGTGCTGTG 540
QY 548 GGCTCCAGCTGCGCTTACCAAGTGTGCGGGGCGCGCGCTGTACCAAGTGTGCGCGCTGCCAC 607
Db 541 GGCTCCAGCTGCGCTTACCAAGTGTGCGGGGCGCGCGCTGTACCAAGTGTGCGCGCTGCCAC 600
QY 608 TCAGGCCCGGCGCGCACACGCTAGTGAACCCGGAAGGCGTGTGGATGGCAAGGCG 667

QY	2792	GCCGGCCACAGGCGCTATTCCCTTGCTGGCTGCTGCTGGATACCCGGACCTGAGGT	2851
Db	2821	GGCGGCCACAGGCGCTATTCCCTTGCTGGCTGCTGCTGGATACCCGGACCTGAGGT	2880
QY	2852	GCAGAGCGACTACTCCAGCTATGCCCCGGAGCTCCATCAGAGCCAGTCTCACCCTCAACCG	2911
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCCGGAGCTCCATCAGAGCCAGTCTCACCCTCAACCG	2940
QY	2912	CGCGTCAAGAGCTGGGGAGAACATGCGTGGCAACTCTTGGGGGTCTTGGCGTGAAGT	2971
Db	2941	CGCGTCAAGAGCTGGGGAGAACATGCGTGGCAACTCTTGGGGGTCTTGGCGTGAAGT	3000
QY	2972	TCACAGCCTGTTCCTGATTTGCAAGTGAACAGCCTCCAGACGGTGTGACCAACATCTA	3031
Db	3001	TCACAGCCTGTTCCTGATTTGCAAGTGAACAGCCTCCAGACGGTGTGACCAACATCTA	3060
QY	3032	CAGATTCCTCTGCTGCGAGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA	3091
Db	3061	CAGATTCCTCTGCTGCGAGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA	3120
QY	3092	TCAGCAAGTTTGAAGAACCCCACTTTTCTCGCGGTCACTCTGACAGGCGCTCCCT	3151
Db	3121	TCAGCAAGTTTGAAGAACCCCACTTTTCTCGCGGTCACTCTGACAGGCGCTCCCT	3180
QY	3152	CTGCTACTCCATCTGAAAGCCAGAACGCGAGGGATGTGCTGGGGCCAAAGGGCGCG	3211
Db	3181	CTGCTACTCCATCTGAAAGCCAGAACGCGAGGGATGTGCTGGGGCCAAAGGGCGCG	3240
QY	3212	CGGCGCTCTGCGCTCCGAGGCGGTGCAGTGGGTGTCACACAAACATTCCTGCTCAAGT	3271
Db	3241	CGGCGCTCTGCGCTCCGAGGCGGTGCAGTGGGTGTCACACAAACATTCCTGCTCAAGT	3300
QY	3272	GACTCGACACCGGTGTACCTAGCTGCGACATCTGGGGTCACTCAGGACAGCCAG - ACG	3330
Db	3301	GACTCGACACCGGTGTACCTAGCTGCGACATCTGGGGTCACTCAGGACAGCCAGTACGC	3360
QY	3331	AGCTGAGTGGGAAGCTCCCGGGAGCAGCGTGACTGCCCTGGAGAGCCGACCCACCCG	3390
Db	3361	AGCTGAGTGGGAAGCTCCCGGGAGCAGCGTGACTGCCCTGGAGAGCCGACCCACCCG	3420
QY	3391	CAGTGCCTCAGACTTCAAGACATCTGTGATGATGAGCCACCGCCACAGCCAGCGG	3450
Db	3421	CAGTGCCTCAGACTTCAAGACATCTGTGATGATGAGCCACCGCCACAGCCAGCGG	3480
QY	3451	AGAGCAGACACACAGCAGCCCTGTACGCGCGGCTCTACGTCCAGAGGAGAGGGCGGC	3510
Db	3481	AGAGCAGACACACAGCAGCCCTGTACGCGCGGCTCTACGTCCAGAGGAGAGGGCGGC	3540
QY	3511	CCACACCCAGGCGCCGACCGCTGGGAGTCTGAGGCGCTGAGTGAAGTGTGGCCGAGGCT	3570
Db	3541	CCACACCCAGGCGCCGACCGCTGGGAGTCTGAGGCGCTGAGTGAAGTGTGGCCGAGGCT	3600
QY	3571	GCATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGC	3630
Db	3601	GCATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGC	3660
QY	3631	TGAGTGTCCAGCACACCTGCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCC	3690
Db	3661	TGAGTGTCCAGCACACCTGCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCC	3720
QY	3691	AGGGCCAGCTTTTCTCTCACACAGAGCCCGGCTTCCACATCCCCACATAGGAATAGTCCATC	3750
Db	3721	AGGGCCAGCTTTTCTCTCACACAGAGCCCGGCTTCCACATCCCCACATAGGAATAGTCCATC	3780
QY	3751	CCAGATTCGCCATTTGTTCACCCCTGCGCTCGCCCTCTTGGCTTCCACCCCCACCAATC	3810
Db	3781	CCAGATTCGCCATTTGTTCACCCCTGCGCTCGCCCTCTTGGCTTCCACCCCCACCAATC	3840
QY	3811	CAGGTGAGACCTTGAGAAGACCTGGGAGCTCTGGAAATTTGAGTGAACCAAGGTCT	3870
Db	3841	CAGGTGAGACCTTGAGAAGACCTGGGAGCTCTGGAAATTTGAGTGAACCAAGGTCT	3900

QY	3871	GCCTGTACACAGGCGCAGACCCTTCACCTGGATGGGGTCCCTGTGGCTCAAATTGGGG	3930
Db	3901	GCCCTGTACACAGGCGCAGACCCTTCACCTGGATGGGGTCCCTGTGGCTCAAATTGGGG	3960
QY	3931	GGAGTGCTGTGGGAGTAATAATACTGAATATATAGATTTTTTCAGTTTTGAAAAAAA	3986
Db	3961	GGAAGTGCTGTGGGAGTAATAATACTGAATATATAGATTTTTTCAGTTTTGAAAAAAA	4016
 RESULT 14 US-09-108-401A-1			
; Sequence 1, Application US/09108401A			
; GENERAL INFORMATION:			
; APPLICANT: Kilian, Andrzej			
; APPLICANT: Bowtell, David			
; TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES			
; FILE REFERENCE: 082447-0103			
; CURRENT APPLICATION NUMBER: US/09/108,401A			
; CURRENT FILING DATE: 1998-06-30			
; NUMBER OF SEQ ID NOS: 155			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 3964			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-108-401A-1			
 Query Match 97.7%; Score 3914.8; DB 6; Length 3964;			
Best Local Similarity 99.0%; Pred. No. 1.6e-109;			
Matches 3926; Conservative 0; Mismatches 2; Indels 36; Gaps			
QY	63	ATGCCGCGCGCTCCCGCGCTGCGGACCGGTGGCGTCCCTGGTGGCAGCCACTACCGCGAG	122
Db	1	ATGCCGCGCGCTCCCGCGCTGCGGACCGGTGGCGTCCCTGGTGGCAGCCACTACCGCGAG	60
QY	123	GTCCTGCGCGTGGCCACAGTTGTTGGGGCGCTGGGGCCCCAGGGCTGGCGCTGTGCAG	182
Db	61	GTGCTGCGCGTGGCCACAGTTGTTGGGGCGCTGGGGCCCCAGGGCTGGCGCTGTGCAG	120
QY	183	CGCGGGGACCGCGCGGCTTTCGCGCGCTGTGGGCCCAAGTGCCTGTGTGCGTGCCTGG	242
Db	121	CGCGGGGACCGCGCGGCTTTCGCGCGCTGTGGGCCCAAGTGCCTGTGTGCGTGCCTGG	180
QY	243	GACGACGGCG	302
Db	181	GACGACGGCG	240
QY	303	GTGGCGCGAGTGTGTGACAGAGGCTGTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG	362
Db	241	GTGGCGCGAGTGTGTGACAGAGGCTGTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG	300
QY	363	TTCGCGCTGTGGACGGGGCGCGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	422
Db	301	TTCGCGCTGTGGACGGGGCGCGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	360
QY	423	AGCTACCTGCCCCAACACAGGTGACGACGACATGCGGGGGAGCGGGGGCGTGGGGCTGCTG	482
Db	361	AGCTACCTGCCCCAACACAGGTGACGACGACATGCGGGGGAGCGGGGGCGTGGGGCTGCTG	420
QY	483	CTGCGCGCGGTGGGCGACGACGCTGTGTTACCTGTGCGCACGCTGCGCGCTTTTGTG	542
Db	421	TTGCGCGCGGTGGGCGACGACGCTGTGTTACCTGTGCGCACGCTGCGCGCTTTTGTG	480
QY	543	CTGGTGGCTTCCAGCTGCGCTTACCAAGGTGTGCGGGGGCGCGCGCTGTACACAGCTGGCGCT	602
Db	481	CTGGTGGCTTCCAGCTGCGCGCTTACCAAGGTGTGCGGGGGCGCGCGCTGTACACAGCTGGCGCT	540
QY	603	GCCACTCAGGCCCGCGCGCGCGCACACGCTAGTTGGACCCCGAAGGCGTGGGATGCGAA	662
Db	541	GCCACTCAGGCCCGCGCGCGCGCACACGCTAGTTGGACCCCGAAGGCGTGGGATGCGAA	600
QY	663	CGGGCCTGGAACCATAGCTCAGGAGGCGGGGCTCCCTTGGGCTGTCCAGCCCGGGGT	722

Db 601 CGGGCTGAACCATAGCTCAGGAGGCGGGGTCCCTGGGCTGCCAGCCCGGGT 660
 QY 723 GCGAGAGGCGGGGCGAGTGCAGCCGAAGTCTGCCGTGGCCAGAGGCCCGCGT 782
 Db 661 GCGAGAGGCGGGGCGAGTGCAGCCGAAGTCTGCCGTGGCCAGAGGCCCGCGT 720
 QY 783 GCGGCTGCCCCGTGAGCCGAGCGGAGCGCCCGTTGGCGAGGGGTCTGGGCCACCCGGC 842
 Db 721 GCGGCTGCCCCGTGAGCCGAGCGGAGCGCCCGTTGGCGAGGGGTCTGGGCCACCCGGC 780
 QY 843 AGGACGCGTGACCGAGTGAACCGTGGTTTCTGTGTGTCTACCTGCCAGACCCCGCGAA 902
 Db 781 AGGACGCGTGACCGAGTGAACCGTGGTTTCTGTGTGTCTACCTGCCAGACCCCGCGAA 840
 QY 903 GAAGCCACCTCTTGTGAGGTGGCGCTCTGTGGCAGCGGCCACTCCACCCATCCGTGGC 962
 Db 841 GAAGCCACCTCTTGTGAGGTGGCGCTCTGTGGCAGCGGCCACTCCACCCATCCGTGGC 900
 QY 963 GCGCAGCACCGCGGGGGCCCCATCCACATCGCGGCCACACGTCCTGGGACACGCT 1022
 Db 901 GCGCAGCACCGCGGGGGCCCCATCCACATCGCGGCCACACGTCCTGGGACACGCT 960
 QY 1023 TGTCCCCCGGTGTACGCGCGAGACCAAGCATTCTCTACTCTCAGGCGACAAGAGCAG 1082
 Db 961 TGTCCCCCGGTGTACGCGCGAGACCAAGCATTCTCTACTCTCAGGCGACAAGAGCAG 1020
 QY 1083 CTGCGGCTCTCTCTACTCTCAGCTCTCTGAGGCCAGCCTGACTGGCGTCGAGGCTC 1142
 Db 1021 CTGCGGCTCTCTCTACTCTCAGCTCTCTGAGGCCAGCCTGACTGGCGTCGAGGCTC 1080
 QY 1143 GTGAGACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGAGGTTGCC 1202
 Db 1081 GTGAGACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGAGGTTGCC 1140
 QY 1203 CGCGTCCCCAGCGCTACTGGCAATGCGGGCGCTGTCTGAGAGCTGCTTGGGAACCA 1262
 Db 1141 CGCGTCCCCAGCGCTACTGGCAATGCGGGCGCTGTCTGAGAGCTGCTTGGGAACCA 1200
 QY 1263 GCGCAGTCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGGGTCA 1322
 Db 1201 GCGCAGTCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGGGTCA 1260
 QY 1323 CCAGCAGCCGCTGTCTGTGCGCGGAGAAAGCCAGGCGCTGTGCGGGCGCCGAGAG 1382
 Db 1261 CCAGCAGCCGCTGTCTGTGCGCGGAGAAAGCCAGGCGCTGTGCGGGCGCCGAGAG 1320
 QY 1383 GAGGACACAGACCCCGCTGCGCTGTGAGCTGCTCCGCCAGACAGACGCCCTGGCAG 1442
 Db 1321 GAGGACACAGACCCCGCTGCGCTGTGAGCTGCTCCGCCAGACAGACGCCCTGGCAG 1380
 QY 1443 GTGTACGGCTTGTGCGGGCTGCGCTGCGCGCGCGGCTGTGCTCCCGAGGCCCTTGGGCTCC 1502
 Db 1381 GTGTACGGCTTGTGCGGGCTGCGCTGCGCGCGCGGCTGTGCTCCCGAGGCCCTTGGGCTCC 1440
 QY 1503 AGGCAACAAGAACGCGCTTCTCAGGAAACACCAAGAGTTCTCTCCCTGGGAAAGCAT 1562
 Db 1441 AGGCAACAAGAACGCGCTTCTCAGGAAACACCAAGAGTTCTCTCCCTGGGAAAGCAT 1500
 QY 1563 GCCAAGCTCTGCTGACAGAGCTGACGTGGAAGATGAGCGTGGCGACTGCGCTTGGCTG 1622
 Db 1501 GCCAAGCTCTGCTGACAGAGCTGACGTGGAAGATGAGCGTGGCGACTGCGCTTGGCTG 1560
 QY 1623 CGCAGAGCCCGAGGGGTGGCTGTCTCCGGCCGACAGACACCGTCTGCGTGAGAGATC 1682
 Db 1561 CGCAGAGCCCGAGGGGTGGCTGTCTCCGGCCGACAGACACCGTCTGCGTGAGAGATC 1620
 QY 1683 CTGGCCAAGTCTCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTTTTC 1742
 Db 1621 CTGGCCAAGTCTCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTTTTC 1680
 QY 1743 TTTTATGTACGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTTC 1802
 Db 1743 TTTTATGTACGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTTC 1802

Db 1681 TTTTATGTACGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTTC 1740
 QY 1803 TGGACCAAGTTGCAAAAGCATTGAATCAGACAGCAGTGAAGAGGCTGACGTGCGGAG 1862
 Db 1741 TGGACCAAGTTGCAAAAGCATTGAATCAGACAGCAGTGAAGAGGCTGACGTGCGGAG 1800
 QY 1863 CTGTGGAAGCAGAGGTCAGGAGCATCGGGAAGCCAGGCCCTGCTGAGCTGACGTCAGA 1922
 Db 1801 CTGTGGAAGCAGAGGTCAGGAGCATCGGGAAGCCAGGCCCTGCTGAGCTGACGTCAGA 1860
 QY 1923 CTCCGCTTCATCCCAAGCCTGACGGGGCTGCGGCCGATGTGAACATGACTAGTCGTG 1982
 Db 1861 CTCCGCTTCATCCCAAGCCTGACGGGGCTGCGGCCGATGTGAACATGACTAGTCGTG 1920
 QY 1983 GGAGCCAGAACGTTCCGACAGAGAAAGAGGGCCGAGCGTCTCACCCTGAGGTTGAAGCA 2042
 Db 1921 GGAGCCAGAACGTTCCGACAGAGAAAGAGGGCCGAGCGTCTCACCCTGAGGTTGAAGCA 1980
 QY 2043 CTGTTCAGCGTGTCTCAACTACGAGCGGGCGCGGCCGCCCTCTGGGCGCTCTGTG 2102
 Db 1981 CTGTTCAGCGTGTCTCAACTACGAGCGGGCGCGGCCGCCCTCTGGGCGCTCTGTG 2040
 QY 2103 CTGGGCTTGACGATATCCACAGGGGCTGGCGCACCCTGCTGCTGCTGTGCGGGCCAG 2162
 Db 2041 CTGGGCTTGACGATATCCACAGGGGCTGGCGCACCCTGCTGCTGCTGTGCGGGCCAG 2100
 QY 2163 GACCCGCGCCCTGAGCTGTA-----CATC 2186
 Db 2101 GACCCGCGCCCTGAGCTGTACTTGTCTCAAGGTGATGTGACGGGGCGCTACGACACCATC 2160
 QY 2187 CCCCAGACAGGCTCAGCGAGGTGATCGCCAGCATCATCAAAACCCAGAACAGTACTGC 2246
 Db 2161 CCCCAGACAGGCTCAGCGAGGTGATCGCCAGCATCATCAAAACCCAGAACAGTACTGC 2220
 QY 2247 GTGCTGCGTATGCGGTGTCCAGAGGCCCGCCATGGGCGACGTCGCCAAGGCTTCAAG 2306
 Db 2221 GTGCTGCGTATGCGGTGTCCAGAGGCCCGCCATGGGCGACGTCGCCAAGGCTTCAAG 2280
 QY 2307 AGCCACGCTCTACTCTTGACAGACCTCCAGCCGTACATGCGACAGTCTGCTGCTACCTG 2366
 Db 2281 AGCCACGCTCTACTCTTGACAGACCTCCAGCCGTACATGCGACAGTCTGCTGCTACCTG 2340
 QY 2367 CAGGACACAGCCCGCTGAGGAGTGGCGTGTATCGAGCAGACGCTCCTCCCTGAATGAG 2426
 Db 2341 CAGGACACAGCCCGCTGAGGAGTGGCGTGTATCGAGCAGACGCTCCTCCCTGAATGAG 2400
 QY 2427 GCCAGCAGTGGCTCTTGCAGCTTCTTCTACGCTTCATGTGCCACACGCGCTGCCATC 2486
 Db 2401 GCCAGCAGTGGCTCTTGCAGCTTCTTCTACGCTTCATGTGCCACACGCGCTGCCATC 2460
 QY 2487 AGGGGCAAGTCTTACGTCAGTGCAGAGGGGATCCCGCAGAGGCTTCATCTCTCCAGCTG 2546
 Db 2461 AGGGGCAAGTCTTACGTCAGTGCAGAGGGGATCCCGCAGAGGCTTCATCTCTCCAGCTG 2520
 QY 2547 CTCTGACGCTGTGCTACGGGCGACATGAGAAACAAGCTGTTTGGGGGATTCGGCGGGAC 2606
 Db 2521 CTCTGACGCTGTGCTACGGGCGACATGAGAAACAAGCTGTTTGGGGGATTCGGCGGGAC 2580
 QY 2607 GGGCTGCTCTGCGTTTGGTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCG 2666
 Db 2581 GGGCTGCTCTGCGTTTGGTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCG 2640
 QY 2667 AAAACCTTCTCAGGACCCGTGTCCGAGCTGTCCCTGAGTATGGCTGCGTGGAACCTG 2726
 Db 2641 AAAACCTTCTCAGGACCCGTGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGAACCTG 2700
 QY 2727 CGGAAGCAGTGTGAACCTTCCCTGTAAGAGACGAGGCCCTGGGTGGCACGGCTTTGT 2786
 Db 2701 CGGAAGCAGTGTGAACCTTCCCTGTAAGAGACGAGGCCCTGGGTGGCACGGCTTTGT 2760
 QY 2787 CAGATGCGGCCCCACGGCTATTCCTGCTGCTGCGGCGCTGCTGCTGATACCCGAGCCTG 2846
 Db 2761 CAGATGCGGCCCCACGGCTATTCCTGCTGCTGCGGCGCTGCTGCTGATACCCGAGCCTG 2820

QY	2847	GAGGTGCAGAGCGGAGCTACTCTCCAGCTATGCCCCGAGACCTTCATATCAGAGCCAGTCTCACCTTC	2906
Db	2821	GAGGTGCAGAGCGGAGCTACTCTCCAGCTATGCCCCGAGACCTTCATATCAGAGCCAGTCTCACCTTC	2880
QY	2907	AACCGGGGCTTCAAGGCTGGGAGGAACATGCCGTCCGAAACTCTTTGGGGTCTTTGGGCTG	2966
Db	2881	AACCGGGGCTTCAAGGCTGGGAGGAACATGCCGTCCGAAACTCTTTGGGGTCTTTGGGCTG	2940
QY	2967	AAGTGTCAACAGCCTGTCTTCTGCAATTTTGCAAGTGAACAGCCTCCAGACGGGTGTGCACCAAC	3026
Db	2941	AAGTGTCAACAGCCTGTCTTCTGCAATTTTGCAAGTGAACAGCCTCCAGACGGGTGTGCACCAAC	3000
QY	3027	ATCTACACAGATCCTCTCTGCTGCAGGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA	3086
Db	3001	ATCTACACAGATCCTCTCTGCTGCAGGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA	3060
QY	3087	TTTCACTCAGCAAGTTTGGAGAAGACCCCACTTTTCTGCGCGTCATCTGTGCACACGGCC	3146
Db	3061	TTTCACTCAGCAAGTTTGGAGAAGACCCCACTTTTCTGCGCGTCATCTGTGCACACGGCC	3120
QY	3147	TCCTCTCTGCTACTCTTCATCTTGAAAGCCCAAGAACGCAAGGATGTGCTGSGGGCCAAAGGC	3206
Db	3121	TCCTCTCTGCTACTCTTCATCTTGAAAGCCCAAGAACGCAAGGATGTGCTGSGGGCCAAAGGC	3180
QY	3207	GCGCGCGGGCCCTGTGCCCTCCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC	3266
Db	3181	GCGCGCGGGCCCTGTGCCCTCCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC	3240
QY	3267	AAGCTGACTCGACACCGTGTCACTACGTGCACTCCTGSGGCTCACTCAGACAGACCCAG	3326
Db	3241	AAGCTGACTCGACACCGTGTCACTACGTGCACTCCTGSGGCTCACTCAGACAGACCCAG	3300
QY	3327	ACGCAAGCTGAGTGGGAAGCTCCCGGGGAGCAGACGCTGACTGCCCCGGAGGGCCGACCAAC	3386
Db	3301	ACGCAAGCTGAGTGGGAAGCTCCCGGGGAGCAGACGCTGACTGCCCCGGAGGGCCGACCAAC	3360
QY	3387	CCGGCACTGCCCTCAGACTTCAAGAACCATCTCTGGACTGATGGCCACCCGCCACAGCCAG	3446
Db	3361	CCGGCACTGCCCTCAGACTTCAAGAACCATCTCTGGACTGATGGCCACCCGCCACAGCCAG	3420
QY	3447	GCCGAGAGCAGACACCAGCAGAGCCCTGTCAACGCGGGCTCTACGTCGCCAGGGAGGAGGGG	3506
Db	3421	GCCGAGAGCAGACACCAGCAGAGCCCTGTCAACGCGGGCTCTACGTCGCCAGGGAGGAGGGG	3480
QY	3507	CGGCCACACACCCAGAGCCCCGCAACCGCTGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAG	3566
Db	3481	CGGCCACACACCCAGAGCCCCGCAACCGCTGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAG	3540
QY	3567	GCCGTGATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGAGTGTCCAGCCAA	3626
Db	3541	GCCGTGATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGCTGAGAGTGTCCAGCCAA	3600
QY	3627	GGGTGAGTGTCCAGCACACACCTGCCGCTTTCACCTTCCACACAGGCTGGCGCTCGGCTCCA	3686
Db	3601	GGGTGAGTGTCCAGCACACACCTGCCGCTTTCACCTTCCACACAGGCTGGCGCTCGGCTCCA	3660
QY	3687	CCCGAGGGCCAGCTTTTCTCTCAACAGAGACCGCGCTTCCACTTCCACCATTAAGGAATAGTC	3746
Db	3661	CCCGAGGGCCAGCTTTTCTCTCAACAGAGACCGCGCTTCCACTTCCACCATTAAGGAATAGTC	3720
QY	3747	CATCCCCAGATTGCCATTTGTTCAACCCCTGCGCTGCCCTCTTGGCTTCCACCCCCAC	3806
Db	3721	CATCCCCAGATTGCCATTTGTTCAACCCCTGCGCTGCCCTCTTGGCTTCCACCCCCAC	3780
QY	3807	CATCCAGGTGAGAACCCCTGAGAAGAACCCCTGGGAGCTCTGGGAATTTGGAGTGAACCAAG	3866
Db	3781	CATCCAGGTGAGAACCCCTGAGAAGAACCCCTGGGAGCTCTGGGAATTTGGAGTGAACCAAG	3840
QY	3867	GTTGGCCCTGTACACAGCGAGAGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATT	3926
Db	3841	GTTGGCCCTGTACACAGCGAGAGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATT	3900

QY	3927	GGGGGGAGGTGCTGTGGAGTAAATACTGAATATATAGCTTTTTCAGTTTGTGAAAAAA	3986
Db	3901	GGGGGGAGGTGCTGTGGAGTAAATACTGAATATATAGCTTTTTCAGTTTGTGAAAAAA	3960
QY	3987	AAAA 3990	
Db	3961	AAAA 3964	
RESULT 15			
	US-09-502-498A-1		
	; Sequence 1, Application US/09502498A		
	; GENERAL INFORMATION:		
	; APPLICANT: Kilian, Andrzej		
	; APPLICANT: Bowtell, David		
	; TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES		
	; TITLE OF INVENTION: THEREOF		
	; FILE REFERENCE: 082447-0102		
	; CURRENT APPLICATION NUMBER: US/09/502,498A		
	; CURRENT FILING DATE: 2000-02-11		
	; NUMBER OF SEQ ID NOS: 155		
	; SOFTWARE: Patentln Ver. 2.0		
	; SEQ ID NO 1		
	; LENGTH: 3964		
	; TYPE: DNA		
	; ORGANISM: Homo sapiens		
	US-09-502-498A-1		
	Query Match	97.7%; Score 3914.8; DB 6; Length 3964;	
	Best Local Similarity	99.0%; Pred. No. 1.6e-109;	
	Matches 3926; Conservative	0; Mismatches 2; Indels 36; Gaps	
QY	63	ATGCGCGCGCTCCCGCTGCGAGCGCTGCGTCCCTGTGCGCAGCCACTACCGGAG	122
Db	1	ATGCGCGCGCTCCCGCTGCGAGCGCTGCGTCCCTGTGCGCAGCCACTACCGGAG	60
QY	123	GTGCTGCCGCTGGCCACAGTTGCTGCGCGCGCTGCGGCCCCAGAGGGCTGCGGCTGTGACAG	182
Db	61	GTGCTGCCGCTGGCCACAGTTGCTGCGCGCGCTGCGGCCCCAGAGGGCTGCGGCTGTGACAG	120
QY	183	CGCGGGGACCGCGGGGCTTCCGCGCGCTGTGCGCCAGTGCCTGTGTGCGCTGCCCTGG	242
Db	121	CGCGGGGACCGCGGGGCTTCCGCGCGCTGTGCGCCAGTGCCTGTGTGCGCTGCCCTGG	180
QY	243	GACGCACGGCGCGCCCCCGCGCGCCCCCTCTCCGCCAGAGTGTCTGCGTGAAGGAGCTG	302
Db	181	GACGCACGGCGCGCCCCCGCGCGCCCCCTCTCTCCGCCAGAGTGTCTGCGTGAAGGAGCTG	240
QY	303	GTCGCCCGAGTGTCTGCAGAGGCTGTGCGAGCGCGCGCGGAGAACGTGCTGGCCTTCGGC	362
Db	241	GTCGCCCGAGTGTCTGCAGAGGCTGTGCGAGCGCGCGCGGAGAACGTGCTGGCCTTCGGC	300
QY	363	TTCGCGCTGTGAGACGGGCGCGCGGGGCCCGCGAGGCGCTTCACCAACAGCGTGGCG	422
Db	301	TTCGCGCTGTGAGACGGGCGCGCGGGGCCCGCGAGGCGCTTCACCAACAGCGTGGCG	360
QY	423	AGCTACCTGCCCCAACACAGGTGACCGACACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG	482
Db	361	AGCTACCTGCCCCAACACAGGTGACCGACACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG	420
QY	483	CTGCGCGCGCTGTGGGCGAGCAGCTGTGTTCACCTGCTGCGCAGCTGCGCGCTCTTGTG	542
Db	421	TTGCGCGCGCTGTGGGCGAGCAGCTGTGTTCACCTGCTGCGCAGCTGCGCGCTCTTGTG	480
QY	543	CTGTGTGCTCCCAAGCTGCGCTTACCAAGGTGTGCGGGCGCGCGCTGTACAGCTCGCGCT	602
Db	481	CTGTGTGCTCCCAAGCTGCGCTTACCAAGGTGTGCGGGCGCGCGCTGTACAGCTCGCGCT	540
QY	603	GCCACTCAGGCCCCCGCCCCCGCCACACGCTAGTGTGACCCCGAAGGCGTGTGGGATGCGAA	662
Db	541	GCCACTCAGGCCCCCGCCCCCGCCACACGCTAGTGTGACCCCGAAGGCGTGTGGGATGCGAA	600
QY	663	CGGCGCTGGAACCATAGCGTCAAGGAGCGCGGGTCCCGCTGGGCTGGCCAGCCCGCGGT	722

Db 601 CGGGCTGGAACCATAGCTGAGGAGCCGGGGTCCCTGGGCTGCGAGCCCGGGT 660
QY 723 GCGAGAGGCGGGGGCAGTGCACGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGCGT 782
Db 661 GCGAGAGGCGGGGGCAGTGCACGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGCGT 720
QY 783 GCGCTGCCCCGTGAGCCGGAGCGGCCGTTGGCAGGGGTCTGGGCCACCCGGGC 842
Db 721 GCGCTGCCCCGTGAGCCGGAGCGGCCGTTGGCAGGGGTCTGGGCCACCCGGGC 780
QY 843 AGGACGCGTGAACCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCAGACC CGCGAA 902
Db 781 AGGACGCGTGAACCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCAGACC CGCGAA 840
QY 903 GAAGCACCCTTTGGAGGGTGGCTCTGTGCACGCGCCACTGCCACCCATCCGTGGC 962
Db 841 GAAGCACCCTTTGGAGGGTGGCTCTGTGCACGCGCCACTGCCACCCATCCGTGGC 900
QY 963 CGCAGACACACGCGGGCCCCCAATCCATCGCGCCACACAGTCCCTGGGACAGCCT 1022
Db 901 CGCAGACACACGCGGGCCCCCAATCCATCGCGCCACACAGTCCCTGGGACAGCCT 960
QY 1023 TGTCCCCGGGTGTACGCCGAGACCAACACTTCTCTACTCTCAGCGCAGACAAGAGCAG 1082
Db 961 TGTCCCCGGGTGTACGCCGAGACCAACACTTCTCTACTCTCAGCGCAGACAAGAGCAG 1020
QY 1083 CTGCGGCCCTCTCTCTACTCAGCTCTGTGAGGCCACGCTGAGTGGCGCTCGAGGCTC 1142
Db 1021 CTGCGGCCCTCTCTCTACTCAGCTCTGTGAGGCCACGCTGAGTGGCGCTCGAGGCTC 1080
QY 1143 GTGAGACCATCTTCTGTGGTTCAGGCCCCCTGGATGCCAGGACTCCCGCAGGTTGCC 1202
Db 1081 GTGAGACCATCTTCTGTGGTTCAGGCCCCCTGGATGCCAGGACTCCCGCAGGTTGCC 1140
QY 1203 CGCTGCCCCAGCGCTACTGGAATGCGGCCCTGTTCTGAGCTGTGGAAACAC 1262
Db 1141 CGCTGCCCCAGCGCTACTGGAATGCGGCCCTGTTCTGAGCTGTGGAAACAC 1200
QY 1263 GCGCAGTCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGTCAAC 1322
Db 1201 GCGCAGTCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGTCAAC 1260
QY 1323 CCAGACGCGGTGTGTGTGCCGGGAGAAGCCCCAGGGCTCTGTGGCGGGCCCCCGAGAG 1382
Db 1261 CCAGACGCGGTGTGTGTGCCGGGAGAAGCCCCAGGGCTCTGTGGCGGGCCCCCGAGAG 1320
QY 1383 GAGGACACAGACCCCCGCTGCCGTGTGCACTGTCTCCGCCAGACAGCAGCCCCCTGGCAG 1442
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QY 1443 GTGTACGGCTTCTGTGGGGCTGCTGCCCGGGCTGGTGGCCCCAGGCCCTCTGGGGCTCC 1502
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QY 1503 AGGCACAACGAACGCCGCTTCTCAGGAACACCAAGAATTCTCTCCCTGGGGAAGCAT 1562
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Db 1501 GCCAAGCTCTGCTGAGAGAGTGAAGTGAAGATGAGCGTGGCGGAAGTGGCTGCTG 1560
QY 1623 CGCAGAGCCCAAGGGTGGCTGTCTCCGGCCGAGAGACACGCTGCGTGAGAGATC 1682
Db 1561 CGCAGAGCCCAAGGGTGGCTGTCTCCGGCCGAGAGACACGCTGCGTGAGAGATC 1620
QY 1683 CTGGCCAAGTCTCTGCACTGGCTGATGAGTGTGTACGTCGTGCACTGCTCAGGCTTTTC 1742
Db 1621 CTGGCCAAGTCTCTGCACTGGCTGATGAGTGTGTACGTCGTGCACTGCTCAGGCTTTTC 1680
QY 1743 TTTTATGTCAAGGAGACACGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTG 1802
|||||

Db 1681 TTTTATGTCAAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTG 1740
QY 1803 TGGAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGGGAG 1862
Db 1741 TGGAGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGGGAG 1800
QY 1863 CTGTGGAAGCAGAGGTTCAGGACAGCATCGGGAAGCCAGGCCCGCTGTGACGTCCAGA 1922
Db 1801 CTGTGGAAGCAGAGGTTCAGGACAGCATCGGGAAGCCAGGCCCGCTGTGACGTCCAGA 1860
QY 1923 CTCCGTTTATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGACTACGTCTG 1982
Db 1861 CTCCGTTTATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGACTACGTCTG 1920
QY 1983 GGAGCCAGAACGTCCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGCA 2042
Db 1921 GGAGCCAGAACGTCCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGCA 1980
QY 2043 CTGTTACGCTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGCGCTCTGTG 2102
Db 1981 CTGTTACGCTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGCGCTCTGTG 2040
QY 2103 CTGGGCTGGAAGATATCCACAGGGCTGGCGCACCTTCTGTGCTGTGCGGGCCAG 2162
Db 2041 CTGGGCTGGAAGATATCCACAGGGCTGGCGCACCTTCTGTGCTGTGCGGGCCAG 2100
QY 2163 GACCCGCGCCTGAGCTGA-----CATC 2186
Db 2101 GACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACCATC 2160
QY 2187 CCCCAGACAGGCTCACGAGGTCAATCGCCAGCATCATCAACCCCAAGAACAGTACTGC 2246
Db 2161 CCCCAGACAGGCTCACGAGGTCAATCGCCAGCATCATCAACCCCAAGAACAGTACTGC 2220
QY 2247 GTGCGTGGTATGCCGTGTGCCAAGAGCCGCCCATGGGCACGTCCGCAAGGCTTCAAG 2306
Db 2221 GTGCGTGGTATGCCGTGTGCCAAGAGCCGCCCATGGGCACGTCCGCAAGGCTTCAAG 2280
QY 2307 AGCCACGTCTTCACTTGACAGACCTTCAAGCCGTACATGCGACAGTTCGTGGCTACCTG 2366
Db 2281 AGCCACGTCTTCACTTGACAGACCTTCAAGCCGTACATGCGACAGTTCGTGGCTACCTG 2340
QY 2367 CAGGACAGAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCCCTGAATGAG 2426
Db 2341 CAGGACAGAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCCCTGAATGAG 2400
QY 2427 GCCAGCAGTGGCTCTTTCAGCGTCTTCTACGCTTCATGTGCCACCAAGCGGTGCCATC 2486
Db 2401 GCCAGCAGTGGCTCTTTCAGCGTCTTCTACGCTTCATGTGCCACCAAGCGGTGCCATC 2460
QY 2487 AGGGCAAGTCTTACGTCCAGTGCAGGGGATCCCGCAGAGGCTCCATCTCTCCACGCTG 2546
Db 2461 AGGGCAAGTCTTACGTCCAGTGCAGGGGATCCCGCAGAGGCTCCATCTCTCCACGCTG 2520
QY 2547 CTCTGACGCTGTGCTACGGCGACATGGAACAAGCTGTTGGGGGATTCGGCGGGAC 2606
Db 2521 CTCTGACGCTGTGCTACGGCGACATGGAACAAGCTGTTGGGGGATTCGGCGGGAC 2580
QY 2607 GGGCTGCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACGCG 2666
Db 2581 GGGCTGCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACGCG 2640
QY 2667 AAAACCTTCTCAGGACCTGTGTCGAGGTTCCCTGAGTATGCGTGGTGAACCTG 2726
Db 2641 AAAACCTTCTCAGGACCTGTGTCGAGGTTCCCTGAGTATGCGTGGTGAACCTG 2700
QY 2727 CGGAAGCAGTGTGAACCTTCCCTGAGAAGACGAGGCCCTGGGTGACAGGCTTTGT 2786
Db 2701 CGGAAGCAGTGTGAACCTTCCCTGAGAAGACGAGGCCCTGGGTGACAGGCTTTGT 2760
QY 2787 CAGATGCGGGCCACAGGCTATTCCTGTGTGCGGCTGCTGATACCCGGAACCTG 2846
Db 2761 CAGATGCGGGCCACAGGCTATTCCTGTGTGCGGCTGCTGATACCCGGAACCTG 2820
|||||

QY	2847	GAGGTGCAGAGGACTACTCTCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCCTTC	2908
Db	2821	GAGGTGCAGAGGACTACTCTCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCCTTC	2880
QY	2907	AACCCGCGCTTCAAGGCTGGGAGGAACATGGCTCGCAAACTCTTTGGGGCTTTGGCGCTG	2966
Db	2881	AACCCGCGCTTCAAGGCTGGGAGGAACATGGCTCGCAAACTCTTTGGGGCTTTGGCGCTG	2940
QY	2967	AAGTGTCAACAGCCTGTTTCTTGATTTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC	3026
Db	2941	AAGTGTCAACAGCCTGTTTCTTGATTTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC	3000
QY	3027	ATCTACAAGATCCTCTGCTGAGGCGGTACAGCTTTACAGCATGTGTGCTGCAGCTCCA	3086
Db	3001	ATCTACAAGATCCTCTGCTGAGGCGGTACAGCTTTACAGCATGTGTGCTGCAGCTCCA	3060
QY	3087	TTTCATCAGCAAGTTTGGAGAACCACACATTTTTCCTGGCGTCACTCTCAGACGGCC	3146
Db	3061	TTTCATCAGCAAGTTTGGAGAACCACACATTTTTCCTGGCGTCACTCTCAGACGGCC	3120
QY	3147	TCCCTCTGCTACTCCATCTCCTGAAAGCCAAAGACGCAGGATGTGCTGGGGCCAAAGGC	3206
Db	3121	TCCCTCTGCTACTCCATCTCCTGAAAGCCAAAGACGCAGGATGTGCTGGGGCCAAAGGC	3180
QY	3207	GCCGCGCGCCCTCTGCCCCTCCGAGGCGCTGCAGTGGCTGTGCCACCAAGCATTTCTGCTC	3266
Db	3181	GCCGCGCGCCCTCTGCCCCTCCGAGGCGCTGCAGTGGCTGTGCCACCAAGCATTTCTGCTC	3240
QY	3267	AACTGACTGCACACCCTGTGCACCTACGTGCCACTCTCTGGGGTCACTCAGAGACGCCCAAG	3326
Db	3241	AACTGACTGCACACCCTGTGTCACTACCTACGTGCCACTCTCTGGGGTCACTCAGAGACGCCCAAG	3300
QY	3327	ACGCAGCTGATTCGGGAAGCTCCCCGGGACGACAGCTGACTGCCCCTGAGGGCCGACGCCAAC	3386
Db	3301	ACGCAGCTGATTCGGGAAGCTCCCCGGGACGACAGCTGACTGCCCCTGAGGGCCGACGCCAAC	3360
QY	3387	CGGCACTGCCCCAGACTTCGAAGACCATCTGTGACTGATGGCCACC CGCCACAGCCAG	3446
Db	3361	CGGCACTGCCCCAGACTTCGAAGACCATCTGTGACTGATGGCCACC CGCCACAGCCAG	3420
QY	3447	GCCGAGAGCAGACACCAGCAGCCTGTGCACGCGCGGCTCTACGTCCACAGGAGGAGGGG	3506
Db	3421	GCCGAGAGCAGACACCAGCAGCCTGTGCACGCGCGGCTCTACGTCCACAGGAGGAGGGG	3480
QY	3507	CGGCCCCACACCAGGCGCCGCAACC GCTGGAGTCTGAGGCGCTGAGTGTTTGGCCGAG	3566
Db	3481	CGGCCCCACACCAGGCGCCGCAACC GCTGGAGTCTGAGGCGCTGAGTGTTTGGCCGAG	3540
QY	3567	GCTTCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAA	3626
Db	3541	GCTTCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAA	3600
QY	3627	GGGCTGAGTGTTCAGCACACACTGCGCTTCTTACTTCCCCACAGGCTGGCGCTCGGCTCCA	3686
Db	3601	GGGCTGAGTGTTCAGCACACACTGCGCTTCTTACTTCCCCACAGGCTGGCGCTCGGCTCCA	3660
QY	3687	CCCCAGGGCAGCTTTTCTCTACACAGAGCGCCGGCTTCCACTCCCCACATPAGGAATAGTC	3746
Db	3661	CCCCAGGGCAGCTTTTCTCTACACAGAGCGCCGGCTTCCACTCCCCACATPAGGAATAGTC	3720
QY	3747	CATCCCCAGATTGCCATTGTTTCAACCCCTGCGCTGCGCTCTTGTGCTTCCACCCCCAC	3806
Db	3721	CATCCCCAGATTGCCATTGTTTCAACCCCTGCGCTGCGCTCTTGTGCTTCCACCCCCAC	3780
QY	3807	CATCCAGGTGAGAACCCCTGAGAAAGGACCCTGGGAGACTCTGGGAATTTGGAGTGACCAAAAG	3866
Db	3781	CATCCAGGTGAGAACCCCTGAGAAAGGACCCTGGGAGACTCTGGGAATTTGGAGTGACCAAAAG	3840
QY	3867	GTTGTCCTGTATACACAGGCGGAGAACCCCTGCACCTGGATGGGGTCCCTGTGGCTCAAAATTT	3926
Db	3841	GTTGTCCTGTATACACAGGCGGAGAACCCCTGCACCTGGATGGGGTCCCTGTGGCTCAAAATTT	3900

[illegible]

Search completed: April 17, 2003, 05:14:37
Job time : 2828 secs

Page 1

GenCore version 5.1.4_p5_4578
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Search time 16 Seconds
(without alignments)
3.976 Million cell updates/sec

US-09-424-686B-1del
4006
1 gttcaagcagcgtctgc.....aaaaaaaaaaaaaaaa 4006

IDENTITY_NUC
Gapop 10.0 , Gapext 0.0
2 seqs, 7940 residues

4

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length: 0
length: 20000000000
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Minimum Match 08

st 2 summaries

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2: /home/sdavid/tmp/apr03/walicka686/align/us-09-108-401a-75:*
*5: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3910	97.6	3918	1	us-09-108-401a-45
2	3900	97.4	4022	2	us-09-108-401a-75

ALIGNMENTS

RESULT 1
us-09-108-401a-45

498

Query Match	97.68;	Score 3910;	DB 1;	length 3918;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 3913; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

[illegible]

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Db	301	TTTGCGCGTGTGTGCACGGGGCGGGGGCCCCCCCCGAGGCTTACCAACCAAGCTGGCC	360
QY	423	AGCTAACCTGCCCAACACGGTGAACCGACGCACTGGCGGGGAGCGGGGCGTGGGGGCTGCTG	482
Db	361	AGCTAACCTGCCCAACACGGTGAACCGACGCACTGGCGGGGAGCGGGGCGTGGGGGCTGCTG	420
QY	483	CTGGCGCGCGTGTGGGCGACGACGTGTGTTCACCTGTGTGCACGCTGCGGCTCTTTGTG	542
Db	421	CTGGCGCGCGTGTGGGCGACGACGTGTGTTCACCTGTGTGCACGCTGCGGCTCTTTGTG	480
QY	543	CTGGTGGCTCCCAAGCTGCGCTTACCAAGTGTGTGGGGCGCGCGCTGTACCAAGCTCGCGCT	602
Db	481	CTGGTGGCTCCCAAGCTGCGCTTACCAAGTGTGTGGGGCGCGCGCTGTACCAAGCTCGCGCT	540
QY	603	GCCACTCAGGCGCGCGCGCGCCGCCACACGCTAGTGGACCCCGAAAGCGTGTGGATGCGAA	662
Db	541	GCCACTCAGGCGCGCGCGCGCGCCGCCACACGCTAGTGGACCCCGAAAGCGTGTGGATGCGAA	600
QY	663	CGGGCCTTGAACCATATAGCGTCAAGGAGGCGCGGGGTCCCGCTGGGCTGCCAGCCCGGCT	722
Db	601	CGGGCCTTGAACCATATAGCGTCAAGGAGGCGCGGGGTCCCGCTGGGCTGCCAGCCCGGCT	660
QY	723	GCGAGGAGGCGCGCGGGGGCAGTGTGCAGCCGAAGTCTGCCCTTGCCCCAAGAAGGCCAGCGT	782
Db	661	GCGAGGAGGCGCGCGGGGGCAGTGTGCAGCCGAAGTCTGCCCTTGCCCCAAGAAGGCCAGCGT	720
QY	783	GCGCCTGCCCCCTGAGCCGAGGCGGACGCCCCGTTGGGAGGGGTCTGGGCGCCACCCGGGC	842
Db	721	GCGCCTGCCCCCTGAGCCGAGGCGGACGCCCCGTTGGGAGGGGTCTGGGCGCCACCCGGGC	780
QY	843	AGGACGCGGTGAGCCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	902
Db	781	AGGACGCGGTGAGCCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	840
QY	903	GAAGCCACCTCTTTGGAGGGTGGCGCTCTGTGCGACGCGGCACTCCACCAATCCGCTGGGC	962
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QY	963	CGCCAGCACCACCGCGGGGGCCCCCATCCACATGCGGGCCACCAAGTCCCTGGGACACGCT	1022
Db	901	CGCCAGCACCACCGCGGGGGCCCCCATCCACATGCGGGCCACCAAGTCCCTGGGACACGCT	960
QY	1023	TGTCCCCCGGTGTACGCGCGAGACCAAGCACTTCTACTCTCTACAGGCGACAAGAGCAG	1082
Db	961	TGTCCCCCGGTGTGTACGCGCGAGACCAAGCACTTCTACTCTCTACAGGCGACAAGAGCAG	1020
QY	1083	CTGGGGCCCTCTCTCTCTACTACTACGCTCTGTGAGGGCCAGGCTGACTGGCGCTGGAGGCTC	1142
Db	1021	CTGGGGCCCTCTCTCTCTACTACTACGCTCTGTGAGGGCCAGGCTGACTGGCGCTGGAGGCTC	1080
QY	1143	GTCGAGACCATCTTTCTGGGTTCAGGCGCCGTGGATGCCAGGGACTCCCGCAGGTGGCC	1202
Db	1081	GTCGAGACCATCTTTCTGGGTTCAGGCGCCGTGGATGCCAGGGACTCCCGCAGGTGGCC	1140
QY	1203	CGCCTGCCCCCAGGCGCTACTGCGCAATGCGGCCCCCTGTTTGTGAGCTGCTTGGGAACCAAC	1262
Db	1141	CGCCTGCCCCCAGGCGCTACTGCGCAATGCGGCCCCCTGTTTGTGAGCTGCTTGGGAACCAAC	1200
QY	1263	GCGCAGTGGCCCTTACGGGGGTGCTCTCAAGAGCGCACTGCCCGCTGCGAGCTGGCGTCAAC	1322
Db	1201	GCGCAGTGGCCCTTACGGGGGTGCTCTCAAGAGCGCACTGCCCGCTGCGAGCTGGCGTCAAC	1260
QY	1323	CCAGCAGCCGCTGTCTGTGCGCGGGAGAAAGCCCCAGGGCTGTGTGGCGGCCCCGAGAGAG	1382
Db	1261	CCAGCAGCCGCTGTCTGTGCGCGGGAGAAAGCCCCAGGGCTGTGTGGCGGCCCCGAGAGAG	1320
QY	1383	GAGGACACAGACCCCCGTGCGCTGTGTGTCAGCTGTCTCGGCAAGCACAGCAGCCCCCTGGCAG	1442

Db 1321 GAGGACACAGACCCCGTCGCCCTGGTGCAGCTGCTCCGCCACAGACAGACGCCCTGGCAG 1380
QY 1443 GTGTACGGCTTCGTGCGGGCCCTGCGCCGGCTGGTGGTCCCCCAGAGCCCTCTGGGGCTCC 1502
Db 1381 GTGTACGGCTTCGTGCGGGCCCTGCGCCGGCTGGTGGTCCCCCAGAGCCCTCTGGGGCTCC 1440
QY 1503 AGGCACACGAACGCCGCTTCTCAGGAACACCAAGAGTTCACTCCCTGGGGAAGCAT 1562
Db 1441 AGGCACACGAACGCCGCTTCTCAGGAACACCAAGAGTTCACTCCCTGGGGAAGCAT 1500
QY 1563 GCCAAGCTCTCGCTGCAGAGAGCTGAGAGATGAGCGTGGGGAAGCTGCGCTTGGCTG 1622
Db 1501 GCCAAGCTCTCGCTGCAGAGAGCTGAGAGATGAGCGTGGGGAAGCTGCGCTTGGCTG 1560
QY 1623 CGCAGAGCCCGAGGGGTTGGCTGTCTCCGGCCGACAGAGACCGTCTGCGTGAGAGATC 1682
Db 1561 CGCAGAGCCCGAGGGGTTGGCTGTCTCCGGCCGACAGAGACCGTCTGCGTGAGAGATC 1620
QY 1683 CTGGCCAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGCTCGAGCTGCTCAGGTCTTTC 1742
Db 1621 CTGGCCAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGCTCGAGCTGCTCAGGTCTTTC 1680
QY 1743 TTTTATGTACGGAGAGACCAGTTCATAAAGAACAAGAGCTCTTTTCTACCGGAAGAGTGT 1802
Db 1681 TTTTATGTACGGAGAGACCAGTTCATAAAGAACAAGAGCTCTTTTCTACCGGAAGAGTGT 1740
QY 1803 TGGAGCAAGTTGCAAAAGCATTTGAATTCAGACAGCAGCTTGAAGAGGTGACGTGGCGAG 1862
Db 1741 TGGAGCAAGTTGCAAAAGCATTTGAATTCAGACAGCAGCTTGAAGAGGTGACGTGGCGAG 1800
QY 1863 CTGTGGAAGCAGAGGTGAGGAGCATGCGGAAGCCAGGCCCTGCTGACGTCCAGA 1922
Db 1801 CTGTGGAAGCAGAGGTGAGGAGCATGCGGAAGCCAGGCCCTGCTGACGTCCAGA 1860
QY 1923 CTCCGTTTCATCCCAAGCCCTGAGCGGCTGCGCCGATTTGACATGAGTACGTGCTG 1982
Db 1861 CTCCGTTTCATCCCAAGCCCTGAGCGGCTGCGCCGATTTGACATGAGTACGTGCTG 1920
QY 1983 GGAGCCAGAAAGCTTCGACAGAAAGAGGGCCGAGCGCTCACTCGAGGAGTGAAGCA 2042
Db 1921 GGAGCCAGAAAGCTTCGACAGAAAGAGGGCCGAGCGCTCACTCGAGGAGTGAAGCA 1980
QY 2043 CTGTTCAGCGTGTCTCACTACGAGCGGGCGGGCCGCTCTGGGGCCTCTGTG 2102
Db 1981 CTGTTCAGCGTGTCTCACTACGAGCGGGCGGGCCGCTCTGGGGCCTCTGTG 2040
QY 2103 CTGGGCTTGGACGATATCCACAGGGCCCTGGCGACCTTCTGCTGCTGTGCGGGCCAG 2162
Db 2041 CTGGGCTTGGACGATATCCACAGGGCCCTGGCGACCTTCTGCTGCTGTGCGGGCCAG 2100
QY 2163 GACCCGCGCGCTGAGCTGTACATCCCCAGGACAGAGGCTCAGGAGGTGATCGCCAGATC 2222
Db 2101 GACCCGCGCGCTGAGCTGTACTTTGTCAAGGACAGGCTCAGGAGGTGATCGCCAGATC 2160
QY 2223 ATCAAAACCCAGAAACAGTACGCTGCGTGGTATGCCGTGCTCCAGAAGGCCGCCAT 2282
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QY 2283 GGGCAGCTCCGCAAGGCCCTTCAAGAGCCAGCTCTTACTTGAACAGCTCCAGGCCGTAC 2342
Db 2221 GGGCAGCTCCGCAAGGCCCTTCAAGAGCCAGCTCTTACTTGAACAGCTCCAGGCCGTAC 2280
QY 2343 ATGCGACAGTTCGTGGCTACCTGCAGGAGACAGCCCGCTGAGGGATGCCGTGCTATC 2402
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QY 2403 GAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCCTTTCAGCTCTTCTACGCTTC 2462
Db 2341 GAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCCTTTCAGCTCTTCTACGCTTC 2400
QY 2463 ATGTGCCACACAGCCGTGGCGATCAGGGGCAAGTCTTACGTCCAGTGGCAGGGATCCCG 2522
Db 2401 ATGTGCCACACAGCCGTGGCGATCAGGGGCAAGTCTTACGTCCAGTGGCAGGGATCCCG 2460

QY 2523 CAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCCTGTGCTACGGCGACATGAGAACAG 2582
Db 2461 CAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCCTGTGCTACGGCGACATGAGAACAG 2520
QY 2583 CTGTTTGGGGGATTCGGCGGGAGCGGCTGCTCTGCGCTTGTGGATGATTTCTTGTG 2642
Db 2521 CTGTTTGGGGGATTCGGCGGGAGCGGCTGCTCTGCGCTTGTGGATGATTTCTTGTG 2580
QY 2643 GTGACACTCACCCTCACCCACGCGGAAAACCTTCTCAGAGACCCTGGTCCGAGGTGCCCT 2702
Db 2581 GTGACACTCACCCTCACCCACGCGGAAAACCTTCTCAGAGACCCTGGTCCGAGGTGCCCT 2640
QY 2703 GAGTATGGCTGCGTGTGAACCTTGGGAAAGACAGTGTGAACCTTCCCTGTAGAAGACAG 2762
Db 2641 GAGTATGGCTGCGTGTGAACCTTGGGAAAGACAGTGTGAACCTTCCCTGTAGAAGACAG 2700
QY 2763 GCCCTGGGTGGCAGCGCTTTTGTTCAGATGCCGGCCACGCGCTATTCCCTGTGGCGGC 2822
Db 2701 GCCCTGGGTGGCAGCGCTTTTGTTCAGATGCCGGCCACGCGCTATTCCCTGTGGCGGC 2760
QY 2823 CTGCTGTGATACCCCGACCCCTGAGAGTGCAGAGCGACTACTCCAGTATGCCCGGACC 2882
Db 2761 CTGCTGTGATACCCCGACCCCTGAGAGTGCAGAGCGACTACTCCAGTATGCCCGGACC 2820
QY 2883 TCCATCAGAGCCAGTCTACCTTCAACCGCGGCTTCAAGGCTGGGAAGAACATGCGTGC 2942
Db 2821 TCCATCAGAGCCAGTCTACCTTCAACCGCGGCTTCAAGGCTGGGAAGAACATGCGTGC 2880
QY 2943 AAACCTTTTGGGGTCTTGGCGGCTGAAGTGTACAGCCCTGTTCTGGATTGACAGGTGAC 3002
Db 2881 AAACCTTTTGGGGTCTTGGCGGCTGAAGTGTACAGCCCTGTTCTGGATTGACAGGTGAC 2940
QY 3003 AGCCTCAGACGGGTGTGACCAACATCTACAAGATCCTCTGCTGACAGGCGTACAGTTT 3062
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QY 3063 CACGCATGTGTCTGACAGTCCCATTTTCATCAGCAAGTTTGAAGAAACCCACATTTTTC 3122
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QY 3123 CTGGCGTCACTCTGACACGGGCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGA 3182
Db 3061 CTGGCGTCACTCTGACACGGGCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGA 3120
QY 3183 GGGATGTGCTGGGGCCAAAGGGCGCGCGGCTGTGCCCTCCGAGGCCGTGACGTGG 3242
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QY 3423 TGATGGCCACCCGCCACAGCCAGGCGGAGAGACAGACACCAAGCCCTGTACGCCGGG 3482
Db 3361 TGATGGCCACCCGCCACAGCCAGGCGGAGAGACAGACACCAAGCCCTGTACGCCGGG 3420
QY 3483 CTCTACGTCCAGGAGGAGGAGGGCGGCCACACACCAAGCCCGCACCGTGGGAGTCTGA 3542
Db 3421 CTCTACGTCCAGGAGGAGGAGGGCGGCCACACACCAAGCCCGCACCGTGGGAGTCTGA 3480
QY 3543 GGCCTGAGTGAAGTGTGGCCGAGGCGCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTG 3602
Db 3481 GGCCTGAGTGAAGTGTGGCCGAGGCGCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTG 3540

QY	3603	AGGCGTAGCGAGTGTGTCCAGCCAAAGSGCTGAGTGTCTCCAGCACACCTGCGGCTCTTCACTTC	3662
Db	3541	AGGCGTAGCGAGTGTGTCCAGCCAAAGSGCTGAGTGTCTCCAGCACACCTGCGGCTCTTCACTTC	3600
QY	3663	CCCACAGGCTGGGCGTGGGCTCCACCCAGGGCCAGCTTTTCCCTCACACAGAGCCCGGCT	3722
Db	3601	CCCACAGGCTGGGCGTGGGCTCCACCCAGGGCCAGCTTTTCCCTCACACAGAGCCCGGCT	3660
QY	3723	TCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTGCGCCTG	3782
Db	3661	TCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTGCGCCTG	3720
QY	3783	CCCTCCTTTGCTTCCACCCCCACCATCCAGTGGAGACCCCTGAGAAGACCCCTGGAGC	3842
Db	3721	CCCTCCTTTGCTTCCACCCCCACCATCCAGTGGAGACCCCTGAGAAGACCCCTGGAGC	3780
QY	3843	TCTGGGAATTTGGAGTGAACCAAAAGTGTGCCCTGTATCACACAGCGAGACCTGCAACCTGG	3902
Db	3781	TCTGGGAATTTGGAGTGAACCAAAAGTGTGCCCTGTATCACACAGCGAGACCCCTGCAACCTGG	3840
QY	3903	ATGGGGGTCCCTGTGGGTCAATTTGGGGGAGGAGTGTCTGTGGGAGTAAATATCTGAATATA	3962
Db	3841	ATGGGGGTCCCTGTGGGTCAATTTGGGGGAGGAGTGTCTGTGGGAGTAAATATCTGAATATA	3900
QY	3963	TGAGTTTTCAGTTTGA	3980
Db	3901	TGAGTTTTCAGTTTGA	3918

RESULT 2
us-09-108-401a-75

Query Match	97.4%;	Score 3900;	DB 2;	Length 4022;
Best Local Similarity	97.3%;	Pred. No. 0;		
Matches 3913; Conservative	0;	Mismatches 5;	Indels 104;	Gaps 1;

[illegible]

Db	541	ACGACGTGCTGTTTCACCTGTGTCACGCTGCGCGCTCTTGTGTGCTGTGCTCCAGCT	600
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Db	601	GGCGCTTACCAAGGTGTGCGGGCGCCGCTGTATACAGCTCGCGGCTGCCACTCAGGCCCGG	660
QY	619	CCCGGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGCGAACGGGCTGGAAACATA	678
Db	661	CCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGCGAACGGGCTGGAAACATA	720
QY	679	GCCTCAGGGAGGCGCGGGTCCCTTGCGCTGCGCAGCCCGCGGTTGCGAGAGCGCGGG	738
Db	721	GCCTCAGGGAGGCGCGGGTCCCTTGCGCTGCGCAGCCCGCGGTTGCGAGAGCGCGGG	780
QY	739	GCAGTGCACAGCCGAAGTCTGCCGTTGCCAAGAAGGCCAGGCGTGGCGTTCCTGAGC	798
Db	781	GCAGTGCACAGCCGAAGTCTGCCGTTGCCAAGAAGGCCAGGCGTGGCGTTCCTGAGC	840
QY	799	CGAGCGGACGCGCGCTTGGCGAGGGGTCTTGCGGCCACCCGCGGCGAGAGCGCTGAGCGA	858
Db	841	CGAGCGGACGCGCGCTTGGCGAGGGGTCTTGCGGCCACCCGCGGCGAGAGCGCTGAGCGA	900
QY	859	GTGACCGTGTGTTCTGTGTGTGTACCTGCCAGACCCCGCGAAGAAGCCACTTTGG	918
Db	901	GTGACCGTGTGTTCTGTGTGTGTACCTGCCAGACCCCGCGAAGAAGCCACTTTGG	960
QY	919	AGGCTGCGCTCTGTGGCACGCGGCCACTCCACCCATCCGTTGGGCGGCAGCACACGCGG	978
Db	961	AGGCTGCGCTCTGTGGCACGCGGCCACTCCACCCATCCGTTGGGCGGCAGCACACGCGG	1020
QY	979	GCCCCCATTCACATCGCGGCCACACAGTCCCTGGGACACGCTTGTCCCGGTGTACG	1038
Db	1021	GCCCCCATTCACATCGCGGCCACACAGTCCCTGGGACACGCTTGTCCCGGTGTACG	1080
QY	1039	CCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGAGCTGCGGCGCTCTTCC	1098
Db	1081	CCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGAGCTGCGGCGCTCTTCC	1140
QY	1099	TACTCAGCTCTCTGAGGCCACAGCTGACTGGCGCTGGAGGCTGTGGAGCACTTTTC	1158
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QY	1159	TGGTTCAGGCGCCCTGGATGCGAGGGACTCCCGCGAGTTGCCCGCGCTGCCAGCGCT	1218
Db	1201	TGGTTCAGGCGCCCTGGATGCGAGGGACTCCCGCGAGTTGCCCGCGCTGCCAGCGCT	1260
QY	1219	ACTGCGAAATGCGCGCCCTGTCTGTGAGCTGCTTGGAAACACGCGAGTGCCTTACG	1278
Db	1261	ACTGCGAAATGCGCGCCCTGTCTGTGAGCTGCTTGGAAACACGCGAGTGCCTTACG	1320
QY	1279	GGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGGGTCAACCCAGCAGCCGCTCT	1338
Db	1321	GGGTGCTCTCTCAAGACGCACTGCCCGCTGCGAGCTGGGTCAACCCAGCAGCCGCTCT	1380
QY	1339	GTGCGCGGAGAGCCCGCAGGCTCTGTGGCGCGCCCGCAGAGGAGAGACAGACCCCC	1398
Db	1381	GTGCGCGGAGAGCCCGCAGGCTCTGTGGCGCGCCCGCAGAGGAGAGACAGACCCCC	1440
QY	1399	GTGCGCTGTGTCAGCTGCTCCGCGCAGCACAGCAGCCCTGGCAGGTGTACGGCTTGTGC	1458
Db	1441	GTGCGCTGTGTCAGCTGCTCCGCGCAGCACAGCAGCCCTGGCAGGTGTACGGCTTGTGC	1500
QY	1459	GGGCGTGCCTGCGCGCGCTGTGTGCCCGCCAGGCGCTCTGGGGCTCCAGGCACAAGAACGCC	1518
Db	1501	GGGCGTGCCTGCGCGCGCTGTGTGCCCGCCAGGCGCTCTGGGGCTCCAGGCACAAGAACGCC	1560
QY	1519	GCTTCTCAGGAACCAAGAAGTTCAATCTCCCTGGGGAAGCATGCCAAGCTCTGCTGC	1578
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Db 1621 AGGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGCCGAGAGAGCCAGGG 1680
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Db 1681 TTGGCTGTGTTCCGGCCGAGACACCGTCTGCGTGAGAGATCCTGGCCAGTTCTTC 1740
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Db 1741 ACTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGTCTTTCTTTATGTACGAGAGA 1800
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Db 1801 CCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAA 1860
QY 1819 GCATTGGAATCAGACAGACACTTGAAGAGGGTGACGCTGGGGAGCTGTGGAAGCAGAG 1878
Db 1861 GCATTGGAATCAGACAGACACTTGAAGAGGGTGACGCTGGGGAGCTGTGGAAGCAGAG 1920
QY 1879 TCAGGCAGCATCGGGAGCGAGCGCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCA 1938
Db 1921 TCAGGCAGCATCGGGAGCGAGCGCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCA 1980
QY 1939 AGCCTGACGGGCTGCGGCCGATTTGTAACATGGACTACGTGTGGAGCCAGAACGTTC 1998
Db 1981 AGCCTGACGGGCTGCGGCCGATTTGTAACATGGACTACGTGTGGAGCCAGAACGTTC 2040
QY 1999 GCAGAGAAAAGAGGGCGCGAGCTCTACCTCGAGGGTGAGGCACTGTTACGCGTCTCA 2058
Db 2041 GCAGAGAAAAGAGGGCGCGAGCTCTACCTCGAGGGTGAGGCACTGTTACGCGTCTCA 2100
QY 2059 ACTACGAGCGGGCGCGCGCCGCCCTCTGCGCGCTCTGTGCTGGGCTGAGCAATA 2118
Db 2101 ACTACGAGCGGGCGCGCGCCGCCCTCTGCGCGCTCTGTGCTGGGCTGAGCAATA 2160
QY 2119 TCCACAGGGGCTGGCGCACCTTCTGTGCTGTGCGGGGCCAGGACCCGCGCTGAGC 2178
Db 2161 TCCACAGGGGCTGGCGCACCTTCTGTGCTGTGCGGGGCCAGGACCCGCGCTGAGC 2220
QY 2179 TGTACATCCCCCAGGACAGGCTCACGGAGGTGTCGCCACATCATCAAAACCCAGACA 2238
Db 2221 TGTACTTTGTCAAGGACAGGCTCACGGAGGTGTCGCCACATCATCAAAACCCAGACA 2280
QY 2239 CGTACTGCGTGGTGGTATGCGGTGTCAGAAAGGCCCATGGGACGTCGCCAAG 2298
Db 2281 CGTACTGCGTGGTGGTATGCGGTGTCAGAAAGGCCCATGGGACGTCGCCAAG 2340
QY 2299 CTTCAAGAGCCACGTCCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGG 2358
Db 2341 CTTCAAGAGCCACGTCCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGG 2400
QY 2359 CTCACCTGCAGAGAGACACCGCGCTGAGGATGCCGTCTCATGAGCAGAGCTCTCC 2418
Db 2401 CTCACCTGCAGAGAGACACCGCGCTGAGGATGCCGTCTCATGAGCAGAGCTCTCC 2460
QY 2419 TGAATGAGGCCAGCAGTGGCTCTTGACGCTTCTCAAGCTTCATGTGCCACACGCG 2478
Db 2461 TGAATGAGGCCAGCAGTGGCTCTTGACGCTTCTCAAGCTTCATGTGCCACACGCG 2520
QY 2479 TGGCATCAGGGGCAAGTCTTACGTCCAGTGGCAGGGATCCCGAGGGCTCCATCTCT 2538
Db 2521 TGGCATCAGGGGCAAGTCTTACGTCCAGTGGCAGGGATCCCGAGGGCTCCATCTCT 2580
QY 2539 CCACGCTGCTGTCAGAGCTGTGCTACGGGCAATGAGAAAGCTGTTGGCGGATTC 2598
Db 2581 CCACGCTGCTGTCAGAGCTGTGCTACGGGCAATGAGAAAGCTGTTGGCGGATTC 2640
QY 2599 GGGCGGAGCGGCTGCTGCTGCTTGGTGATGATTTCTGTTGGTGACACCTCACTCA 2658
Db 2641 GGGCGGAGCGGCTGCTGCTGCTTGGTGATGATTTCTGTTGGTGACACCTCACTCA 2700
QY 2659 CCCACGGGAAAACCTTCCTCAGGACCCCTGTCGAGGTGCCCTGATATGCGTGG 2718
Db 2701 CCCACGGGAAAACCTTCCTCAGGACCCCTGTCGAGGTGCCCTGATATGCGTGG 2760

QY 2719 TGAACCTGCGGAGACAGTGTGAACCTTCCCTGTAGAAGACGAGCCCTGGGTGACGG 2778
Db 2761 TGAACCTGCGGAGACAGTGTGAACCTTCCCTGTAGAAGACGAGCCCTGGGTGACGG 2820
QY 2779 CTTTGTTCAGATGCCGGCCACGGGCTATTCCCTGTGTGGGCTGCTGTGATACCC 2838
Db 2821 CTTTGTTCAGATGCCGGCCACGGGCTATTCCCTGTGTGGGCTGCTGTGATACCC 2880
QY 2839 GGACCCCTGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTC 2898
Db 2881 GGACCCCTGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTC 2940
QY 2899 TCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGCAACTCTTTGGGCTCT 2958
Db 2941 TCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGCAACTCTTTGGGCTCT 3000
QY 2959 TGGGCTGAAGTGTACACAGCTGTTTCTGATTTGACGTGAACAGCCTCCAGAGGCTGT 3018
Db 3001 TGGGCTGAAGTGTACACAGCTGTTTCTGATTTGACGTGAACAGCCTCCAGAGGCTGT 3060
QY 3019 GCACCAACATCTACAAGATCTCTCTGTCGAGGCGTACAGGTTTACAGCATGTGCTGC 3078
Db 3061 GCACCAACATCTACAAGATCTCTCTGTCGAGGCGTACAGGTTTACAGCATGTGCTGC 3120
QY 3079 AGCTCCCATTTTCATCAGCAAGTTTGAAGAACCACATTTTCTGCGGCTCATCTCTG 3138
Db 3121 AGCTCCCATTTTCATCAGCAAGTTTGAAGAACCACATTTTCTGCGGCTCATCTCTG 3180
QY 3139 ACACGGCTCTCCTGTGCTACTTCATCTCTGAAGGCCAAGACGAGGATGTGCTGGGG 3198
Db 3181 ACACGGCTCTCCTGTGCTACTTCATCTCTGAAGGCCAAGACGAGGATGTGCTGGGG 3240
QY 3199 CCAAGGGGCGCGCGGCTCTGCTGCTCCGAGGCGGTCAGTGGCTGTGCCACCAAGCAT 3258
Db 3241 CCAAGGGGCGCGCGGCTCTGCTGCTCCGAGGCGGTCAGTGGCTGTGCCACCAAGCAT 3300
QY 3259 TCCCTGCTCAAGCTGACTGCAACCGTGTACCTACCTACGTGCCACTCTGGGGTCACTAGA 3318
Db 3301 TCCCTGCTCAAGCTGACTGCAACCGTGTACCTACCTACGTGCCACTCTGGGGTCACTAGA 3360
QY 3319 CAGCCAGACGACGCTGATGCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGGGCG 3378
Db 3361 CAGCCAGACGACGCTGATGCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGGGCG 3420
QY 3379 CAGCCAAACCCGGCAGCTGCCCTCAGACTTCAAGACCAATCTGAGTGGCCACCCGCC 3438
Db 3421 CAGCCAAACCCGGCAGCTGCCCTCAGACTTCAAGACCAATCTGAGTGGCCACCCGCC 3480
QY 3439 ACAGCCAGGCGGAGAGCAGACACCAAGACCCCTGTACGCGCGGCTTACGTCCAGGGGA 3498
Db 3481 ACAGCCAGGCGGAGAGCAGACACCAAGACCCCTGTACGCGCGGCTTACGTCCAGGGGA 3540
QY 3499 GGGAGGGGCGGCGCACACCAAGGCCCGCACCGCTGGGAGTCTGAGGCTGAGTGAAGTGT 3558
Db 3541 GGGAGGGGCGGCGCACACCAAGGCCCGCACCGCTGGGAGTCTGAGGCTGAGTGAAGTGT 3600
QY 3559 TGGCCGAGGCTGATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGT 3618
Db 3601 TGGCCGAGGCTGATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGT 3660
QY 3619 CCAGCCAAAGGCTGAGTGTCCAGACACACCTGCCGTCTTCACTTCCACACAGGCTGGCGCT 3678
Db 3661 CCAGCCAAAGGCTGAGTGTCCAGACACACCTGCCGTCTTCACTTCCACACAGGCTGGCGCT 3720
QY 3679 CGGCTCCACCCAGGGGCGCAGCTTTCTCTACACAGAGAGCCGGCTTCCACTCCCAACATAG 3738
Db 3721 CGGCTCCACCCAGGGGCGCAGCTTTCTCTACACAGAGAGCCGGCTTCCACTCCCAACATAG 3780
QY 3739 GAATAGTCCATCCCAAGATTCGCAATTTGTTCACACCCCTGCGCTCTTGGCTTCC 3798
Db 3781 GAATAGTCCATCCCAAGATTCGCAATTTGTTCACACCCCTGCGCTCTTGGCTTCC 3840

OY 3799 ACCCCACCATCCAGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGAAATTGGAGT 3858
Db 3841 ACCCCACCATCCAGGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGAAATTGGAGT 3900
OY 3859 GACCAAAGGTGTGCCCTGTACACAGCGGAGACCCCTGCACCTGGATGGGGTCCCTGTGG 3918
Db 3901 GACCAAAGGTGTGCCCTGTACACAGCGGAGACCCCTGCACCTGGATGGGGTCCCTGTGG 3960
OY 3919 GTCAAATTGGGGAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTCAGTTT 3978
Db 3961 GTCAAATTGGGGAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTCAGTTT 4020
OY 3979 GA 3980
Db 4021 GA 4022

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Job time : 21 secs

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splice variant SEQ1, 2184-2215

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 17, 2003, 16:41:18 ; Search time 4 seconds (without alignments)

2.243 Million cell updates/sec in "401"

Title: us-09-108-401a-46
Perfect score: 5898
Sequence: 1 MPRAPRCRAVRSILRSHYRE.....TALAAANPALPSDFKTIID 1120

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1 segs, 4006 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=soft -O=us-09-108-401a-46 -DB=walicka686.seq
-SUFFIX=ptlo -OUT-align_p_n -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFM=ptlo
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCP=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : walicka686.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5882	99.7	4006	1	US-09-424-686B-1del

ALIGNMENTS

RESULT 1
US-09-424-686B-1del
; Sequence 1, Application US/09424686B
; GENERAL INFORMATION:
; APPLICANT: Hagen, Gustav
; APPLICANT: Siegmund, Hans-Ulrich
; APPLICANT: Weichel, Walter
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
; FILE REFERENCE: Beyer 10,203
; CURRENT APPLICATION NUMBER: US/09/424,686B
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCF/EP98/03468
; PRIOR FILING DATE: 1998-06-09

NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-424-686B-1del

Alignment Scores:

Pred. No.: 0
Score: 5882.00
Length: 4006
Matches: 1117
Percent Similarity: 99.82%
Best Local Similarity: 99.73%
Conservative: 1
Query Match: 99.73%
Mismatches: 2
DB: 1
Indels: 0
Gaps: 0

us-09-108-401a-46 (1-1120) x US-09-424-686B-1del (1-4006)	
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20	
DB 63 ATGCCGCGCGCTCCCGCTGCCGAGCGCGTGCCTGCTGCGCAGCCACTACCGCGAG 122	
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPargLeuValGln 40	
DB 123 GTGCTGCCCTGGCCACGCTTCGTGCGCGCTGGGCGCCAGGGCTGGCGCTGTCAG 182	
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60	
DB 183 CGCGGGAGACCGCGCGCTTCCGCGCGCTGTGCGCCAGTGCTGTGTGTGCGCTGCG 242	
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuTyrGlnLeu 80	
DB 243 GACGACGCGCGCGCGCGCGCGCGCGCTTCCTCCGCAAGTGTCTGCTGCAAGAGACTG 302	
QY 81 ValAlaArgValLeuGlnArgLeuGlyCysGluArgGlyAlaAlaCysValLeuAlaPheGly 100	
DB 303 GTGGCCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGGAGAGAGAGTGTGCTTGGC 362	
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120	
DB 363 TTCCGCGCTGTGACGCGCGCGCGCGCGCGCGCGCGCGCTTCCTCCGCAAGTGTCTG 422	
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140	
DB 423 AGCTACCTGCCACACACGCTGACCGACCTGCGGGGAGCGGGGCTGCTGCTG 482	
QY 141 LeuArgArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160	
DB 483 CTGCGCGCGCTGGCGGCGAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542	
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180	
DB 543 CTGGTGGCTCCACGCTGCGCTTACAGGTGTGCGGGCGCGCTGTACAGCTGCGGCT 602	
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200	
DB 603 GCCACTCAGGCGCGCGCGCGCGCGCTAGTGACCGCGCGAGGCGCTGTGGATGCGAA 662	
QY 201 ArgAlaTyrPasnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220	
DB 663 CGGGCTGTGACCATATAGCTCAGGAGGCGCGGGTCTCCCTGCGGCTGCCAGCGCGGCT 722	
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240	
DB 723 GCGAGGAGCGCGCGCGCGCGCTGCGCGAGGCTGCGCGTGTGCGCAAGAGCGCGAGG 782	
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrPalaHisProGly 260	
DB 783 GCGCGTGCCTGAGCGCGAGCGGAGCGCGCGCTGTGGGAGGCGGTCTGGGCGCGCGGCG 842	
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280	
DB 843 AGGACGCGTGACCGAGTGCCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 902	

QY	281	GIuAlaThrSerLeuGIuGIyAlaLeuSerGIyThrArgHisSerHisProSerValGIy	300
Db	903	GAAGCACCTCTTTGGAGGGTGGCTCTGTGGCAGCGCGCACTCCACCCATCCGTGGGC	962
QY	301	ArgGlnHisHisAlaGIyProProSerThrSerArgProProArgProTrrAspThrPro	320
Db	963	CGCCAGCACACACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGGCT	1022
QY	321	CysProProValTyrAlaGIuThrLysHisPheLeuTyrSerSerGIyAspLysGIuGln	340
Db	1023	TGTTCCTCCCGGTGTACGCGCCGAGACCAAGCACTTCCTCTACTCTCAGCGCACAAGAGCAG	1082
QY	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGIyAlaArgArgLeu	360
Db	1083	CTGGCGGCCCTCTCTCTACTGACTCTGTGAGGCCACGCTGACTGGCGCTGGAGGCTTC	1142
QY	361	ValGIuThrIlePheLeuGIySerArgProTrrMetProGIyThrProArgArgLeuPro	380
Db	1143	GTEGAGACCATCTTCTGTGGTTCAGGCGCCCTGGATGCCAGGACTCCCGCAGGTTGCC	1202
QY	381	ArgLeuProGlnArgTyrTrrPcinMetArgProLeuPheLeuGIuLeuLeuGIyAsnHis	400
Db	1203	CGGCTGCCCGCCAGCGCTACTGGCAATGCGGCCCTGTTCGTGGAGCTGCTTGGGAACAC	1262
QY	401	AlaGlnCysProTyrGIyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
Db	1263	GCGCAGTGCCCCCTACGGGGTCTCTCAAGACGCACTGCCCGCTGGAGCTGGTCAAC	1322
QY	421	ProAlaAlaGIyValCysAlaArgGIuLysProGlnGIySerValAlaAlaProGIuGln	440
Db	1323	CCAGCAGCCGGTGTCTGTGCCCGGAGAGAGCCCGAGGGCTGTGGCGGCCCGCAGAG	1382
QY	441	GIuAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrrPcin	460
Db	1383	GAGGACACAGACCCCGCTGGCTGTGCAGCTGTCCGCCAGACACAGCAGCCCTGGGAG	1442
QY	461	ValTyrGIyPheValArgAlaCysLeuArgArgLeuValProProGIyLeuTrrPcinSer	480
Db	1443	GTTGTACGGCTTCGTGGGGGCTGCCCTGCCCGCGGTGGTCCCCCAGGCTCTGGGGCTCC	1502
QY	481	ArgHisAsnGIuArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGIyLysHis	500
Db	1503	AGGCACACAGACGCGCGCTTCCTCAGGAACACCAAGACTTCATCTCCCTGGGGAGACAT	1562
QY	501	AlaLysLeuSerLeuGlnLeuThrTrrPlyMetSerValArgAspCysAlaTrrPleu	520
Db	1563	GCCAAGCTCTCGCTGCAGAGCTGACGTGAAGATGACGCTGCGGACTGGCGTTGGCTG	1622
QY	521	ArgArgSerProGIyValGIyCysValProAlaAlaGlnHisArgLeuArgGIuGlnIle	540
Db	1623	CGCAGGAGCCACAGGGGTGGCTGTCTCCGCGCGCAGACACCGTCTGCTGAGAGATC	1682
QY	541	LeuAlaLysPheLeuHisTrrPleuMetSerValTyrValValGIuLeuLeuArgSerPhe	560
Db	1683	CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACTGCTCGAGCTGCTCAGGTCTTTC	1742
QY	561	PheTyrValThrGIuThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
Db	1743	TTTTATGTCAAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGTGTTC	1802
QY	581	TrrSerLysLeuGlnSerIleGIyIleArgGlnHisLeuLysArgValGlnLeuArgGln	600
Db	1803	TGGAGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTCGGGAG	1862
QY	601	LeuSerGIuAlaGIuValArgGlnHisArgGIuAlaArgProAlaLeuLeuThrSerArg	620
Db	1863	CTGTGGAAGCAGAGGTTCAGGCACAGCATCGGGAAGCCAGCCCGCTGTCGAGTCCAGA	1922
QY	621	LeuArgPheIleProLysProAspGIyLeuArgProIleValAsnMetAspTyrValVal	640
Db	1923	CTCCGTTTCATCCCCCAACCTGCACGGGCTGCGGCGGATTTGTGAACATGACTACGTCTGTG	1982

QY	641	GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
Dd	1983	GGAGCCAGAACGTTCGCCAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGCA	2042
QY	661	LeuPheSerValLeuAsnTyrgluArgAlaArgArgProglyLeuLeuGlyAlaSerVal	680
Dd	2043	CTGTTCAGCGTGCTCACTACGAGGGGGGGGGCCCCGGGCTCCTGGGGCTGTG	2102
QY	681	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
Dd	2103	CTGGGCGCTGGACGATATCCACAGGGCTGGCCACCCTTCGTCTGCTGCGGGCCAG	2162
QY	701	AspProProGluLeuTyrrPheValLysAspArgLeuThrGluValIleAlaSerIle	720
Dd	2163	GACCCGGCGCTGAGCTGTACATGCCCGCAGACAGGGCTCACGGAGGTCATCGCCAGCATC	2222
QY	721	IleLysProGlnAsnThrTyrcysValArgArgTyrrAlaValalGlnLysAlaAlanis	740
Dd	2223	ATCAAACCCAGAACACGTACTGCGTGCCTGCGTATGCCGTGGTCCAGAAGCGGCCCAT	2282
QY	741	GlyHisValArgLysAlaPheLysSerHisValSerThrLeuThrAspLeuGlnProtyr	760
Dd	2283	GGGCACTCCGCAAGGCCCTTCAGAGCCACGCTCTACTTTGACAGACCTCCAGCCGTAC	2342
QY	761	MetArgGlnPheValAlaHisLeuGlnGluThrSerProLeuArgAspAlaValIle	780
Dd	2343	ATGGACAGTTCTGCTGCTCACCCTGCAGAGACGAGACCCCGTAGGGATGCGTCTCATC	2402
QY	781	GluGlnSerSerSerLeuAsnGluAlaSerSergLyLeuPheAspValPheLeuArgphe	800
Dd	2403	GAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTAGGCCCTTCGACGCTCTCTACGGCTTC	2462
QY	801	MetCysHisHisAlaValArgIleArgGlyLysSerTyrrValGlnCysGlnGlyIlePro	820
Dd	2463	ATGTGCCACACCACGCCGTGCGCATCAGGGGCAAGTCTTACCTCCAGTGCCAGGGGATCCC	2522
QY	821	GlnGlySerIleLeuSerThrLeuLeuCysSerLeuCysTyrglyAspMetGluAsnLys	840
Dd	2523	CAGGGCTCCATCTCTCCACGCTGCTGTGCAGCCTGTGTACGGCGACATGGAGACAAG	2582
QY	841	LeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuLeuArgLeuValAspAspPheLeu	860
Dd	2583	CTGTGTGCGGGATTCGGCGGACGGGCTGCTCTGCGTTTGGTGATGATTCTTGTGTG	2642
QY	861	ValThrProHisLeuThrHisAlaLysThrPheLeuArgThrLeuValArgGlyValPro	880
Dd	2643	GTCGACACCTCACCTCACCCACGCGAAACCTTCTTCAGGACCCCTGGTCCGAGGTTCCT	2702
QY	881	GluTyrglyCysValValAsnLeuArgLysThrValValAsnPheProValGluAspGlu	900
Dd	2703	GAGTATGGCTGCGTGTGAACCTTGGGAAGACAGTGTGAACCTTCCCTGTAGAAAGCGAG	2762
QY	901	AlaLeuGlyGlyThraIaPheValGlnMetProAlaHisGlyLeuPheProTrpCysGly	920
Dd	2763	GCCCTGGGTGGCACGGCTTTTGTTCAGATGCGGGCCACGGCCTATTCCCTGTGTGCGGC	2822
QY	921	LeuLeuLeuAspThrArgThrLeuGluValGlnSerAspTyrSerSerTyrrAlaArgThr	940
Dd	2823	CTGCTGCTGGATACCCGGGACCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCGGAC	2882
QY	941	SerIleArgAlaSerLeuThrPheAsnArgGlyPheLysAlaGlyArgAsnMetArgArg	960
Dd	2883	TCCATCAGAGCCAGTCTCACTTCAACCGCGGCTTCAAGGCTGGAGGAACATGCGTCC	2942
QY	961	LysLeuPheGlyValLeuArgLeuLysCysHisSerLeuPheLeuAspLeuGlnValAsn	980
Dd	2943	AAACTCTTTGGGGCTGTGGGCTGAAGTGTACACAGCCTGTTCTGGATTTCAGGTGAAC	3002
QY	981	SerLeuGlnThrValCysThrAsnIleTyrrLysIleLeuLeuLeuGlnAlaTyrrArgphe	1000
Dd	3003	AGCCTCCAGACGGTGTGCACCAACATCTACAAAGATCTCTCTGTCAGGGCGTAACAGTTT	3062
QY	1001	HisAlaCysValLeuGlnLeuProPheHisGlnGlnValTrpLysAsnProThrPhephe	1020

2 volung
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Db	3063	CACGCATGTGCTGCTGACAGCTCCCATTTTCATCAGCAAGTTTGAAGAACCACACATTTTTC	3122
QY	1021	LeuArgValIleSerAspThrAlaSerLeuCysTyrSerIleLeuLysAlaLysAsnAla	1040
Db	3123	CTGCCGCTCATCTCTGACACGGCCCTCCCTGCTACTTCATCCTGAAGCCCAAGACGCA	3182
QY	1041	GlyMetSerLeuGlyAlaLysGlyAlaAlaGlyProLeuProSerGluAlaValGlnTrp	1060
Db	3183	GGGATGTGCTGGGGGGCCAGAGGGCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGG	3242
QY	1061	LeuCysHisGlnAlaPheLeuLeuLysLeuThrArgHisArgValThrTyrValProLeu	1080
Db	3243	CTGTGCCACCAAGCATTTCTGCTCAAGCTGACTGACACCGGTGTCACTACGTGCCACTC	3302
QY	1081	LeuGlySerLeuArgThrAlaGlnThrGlnLeuSerArgLysLeuProGlyThrThrLeu	1100
Db	3303	CTGGGGTCACTCAGACAGCCAGACGCGCTGAGTCGGAAGCTCCCGGGGACGACGCTG	3362
QY	1101	ThrAlaLeuGluAlaAlaAlaAsnProAlaLeuProSerAspPheLysThrIleLeuAsp	1120
Db	3363	ACTGCCCTGAGGCGCGCAGCCAAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC	3422

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Job time : 17 secs

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